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WPI; 2001-218342/22.
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AAB72500;
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Drosophil
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re greater than or equal to the score of the result being printed,
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(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Match 1
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ALIGNMENTS

ö cell The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient Modulating oxidative stress level in a cell, involves contacting the with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. Gaps ö Length 7; Indels Dermatological; oxidative stress regulator; colostrinin. Query Match 100.0%; Score 42; DB 4; I Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0; Boldogh I; AAB72500 standard; peptide; 7 AA Claim 6; Page 25; 48pp; English 17-AUG-2000; 2000WO-US022665 99US-0149310P entry (TEXA) UNIV TEXAS SYSTEM Hughes TK, Colostrinin peptide #1

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RESULT 2

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AAB59324

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Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
   dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.
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                                                                                                                                                                                                                                                                                                        Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
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Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM.
(REGE-) REGEN THERAPEUTICS PLC.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                              WO200111937-A2
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                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                         regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                           Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
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                                                                                                        AAB59324 standard; peptide; 7 AA.
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Best Local Similarity
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Length 7; Indels

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WO200213849-A1
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                                                                               Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                                                                  differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neural cell differentiation; neural cell regulator; colostrinin peptide; neural cell formation; proline-rich polypeptide aggregate; colostrum; neural cell treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promoting cell differentiation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
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                                                                                                                                                                      The present invention relates to a method for promoting neural cell
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                                                                                                                                         Claim 6; Page 21; 35pp; English
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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. It is classified as having a beta-casein homologue precursor. Methods are claimed for: inducing a cytokine in a cell by contact with an immunological regulator, where the cort is present in a cell culture, a tissue, an organ or an organism, and cell is present in a cell culture, a tissue, an organ or an organism, and cell by contact with the immunological regulator under conditions effective to induce a cytokine, modulating an immune response in a patient by administering an immunological regulator under conditions effective to induce a cytokine, where the immunological regulator is caministered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting consent in a cell culture or an organism, are mammalian or human, and where the blood cells are increased in number or differentiated; and a
                                                                                                                                                                                                                                                                                                                                                         ö
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invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present anino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
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blood cell regulator; cytokine inducer; beta-casein; human.
                                                                                                                                                                                                                                                                                   Length 7;
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Pred. No. 1.8e+06;
O; Mismatches 0;
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Similarity 100.0%;
7; Conservative 0;
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; oxgan; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
method for modulating blood cell proliferation in a patent. A claimed cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and interleukin-12. It was one of the best overall inducers in almost all cytokine and blood cell proliferation experiments conducted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
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                                                                                                                                                                                              Length 7;
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                                                                                                                                                                                          100.0%; Score 42; DB 5; L
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                    AAE20228 standard; peptide; 7 AA.
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                                                                                                                                                      Sequence 7 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of colostrinin for e.g. modulating an intracellular signaling molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4HNE-mediated lipid peroxidation down regulation, apoptosis inhibition, DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor; 4HNE-protein adduct formation reduction; 4HNE-mediated glutathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
enhanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulator; colostrinin; intracellular signaling molecule modulator;
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                                                                                                                                    100.0%; Score 42; DB 5; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        ADN60295 standard; peptide; 7 AA.
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Best Local Similarity 100...
7, Conservative
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STANTON J G.
GEORGIADES J A.
HUGHES T K.
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                                                                                                    7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                         ADN60295;
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Colostrinin, or its constituent peptide or active analogue is useful for inhibiting apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and
                                                                                                                                        Gaps
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                                                                                                            Length 7;
                                                                                                                                       0; Indels
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                                                                                                           100.0%; Score 42; DB 8; I
100.0%; Pred. No. 1.8e+06;
                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                  ADS74400 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polanowski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2003; 2003GB-00005552.
08-MAR-2004; 2004GB-00005190.
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                                                                                                                                       7; Conservative
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                                                                                                                                                                 1 MOPPPLP 7
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MOPPPLP 7
                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004081038-A1.
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                                                                                 Sequence 7 AA;
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ADS74400
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system development of a child's immune system, as a distart such as chart and viral infections, to improve the promote the dissolution of beta-amyloid plaques
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Score 42; DB 8; L
Pred. No. 1.8e+06;
0; Mismatches 0;
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                   AAB59354 standard; peptide; 8 AA.
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Similarity 100.0%;
7; Conservative 0;
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Matches
    Query Match
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Matches 7
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ABB67510
ID ABB675
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AC ABB679
DT 26-MAI
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27-SEP-2001

us-10-691-330-1.rag

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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up of whom-regulated in transgenic plants overexpressing the heterodimeric EZPA/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invantion describes comparing transgenic plants for the production of growth regulators, carymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or complysiology, altered endoreduplication, biochemistry, signal cor physiology, altered mobilization and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or hegative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell can an anticopen and or carbon meterabolism or they function as transcribtion factors. This polypeptide sequence is that cress protein content in plants overexpressing invancion.
                                                                                                                                                                                                                  Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenic virus, alternative reading frame; antigenic determinant, virucide; vaccine; therapeutic agent; infection; HPV.
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                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 564; 134pp; English.
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                                                                                                      Vlieghe
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            18-OCT-2002; 2002EP-00079408.
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                                                                                                      De Veylder L,
                                                        (CROP-) CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 MOPPPMP 658
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N-PSDB; ADN72668.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                              more proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABR2702). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 29322; 21pp + Sequence Listing; English
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Drosophila melanogaster polypeptide SEQ ID NO 29322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN72669 standard; protein; 785 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                Drosophila melanogaster
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nes 7; Conserv
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2003EP-00450171.

11-JUL-2003; 24-JUL-2002;

20-OCT-2003; 2003WO-EP011658

29-APR-2004.

15-JUL-2004

ADN72669;

Query Match

Best Loc Matches

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(INTE-) INTERCELL AG

2002AT-00001124

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06-MAY-2004
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Best Local S
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                                                                                                                        This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the
                                                      New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide encoded by an alternative reading frame of a pathogenic secomprising an antigenic determinant, useful for treating or
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Pred. No. 1.8e+06;
I; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus peptide #2392.
                                                                                                     Claim 18; Page 199; 220pp; English
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            Habel A;
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11-JUL-2003; 2003EP-00450171.
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                                                                                                                                                                                                                                                         Sequence 9 AA;
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production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a mathionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present
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Pred. No. 45;
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                                                                                                                                                                                      Sequence 10 AA;
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Tue Apr 12 09:04:54 2005

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1 LQPPPLP 7

Search completed: April 12, 2005, 08:18:13 Job time : 42.2 secs

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RESULT 2
US-09-270-767-39742

Sequence 39742, Application US/09270767

Sequence 39742, Application US/09270767

Sequence 39742, Application US/09270767

Sequence 39742, Application US/09270767

SENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: 1999-03-17

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 39742

INPE: PRT
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Sequence 54959, A
Sequence 43029, A
Sequence 16, Appl
Sequence 26, Appli
Sequence 6, Appli
Sequence 27326, A
Sequence 31536, A
Sequence 31536, A
Sequence 31536, A
Sequence 18765, A
Sequence 10902, A
Sequence 10902, A
Sequence 10902, A
Sequence 10194, A
Sequence 71, Appl
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61, Appl
23236, A
9, Appli
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34, Appl
34, Appl
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                                                                                                      April 12, 2005, 07:49:30 ; Search time 8.20909 Seconds (without alignments) 63.654 Million cell updates/sec
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-270-767-39742

US-09-270-767-43029

US-08-339-214-16

US-08-339-214-26

US-09-246-129B-6

US-09-246-129B-6

US-09-246-129B-6

US-09-248-796A-27326

US-09-248-796A-18765

US-09-252-91A-3139

US-09-252-91A-3139

US-09-252-91A-3139

US-09-253-91A-3104

US-09-391-0137

US-09-949-016-10902

US-09-949-018-270-34
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US-09-248-796A-23236
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                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence 1, Application US/09641803
Sequence 1, Application US/09641803
Fatest No. 6500798
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: BOLDOGH, ISEVAN
ITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
ITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: A65.00220101
CURRENT APPLICATION NUMBER: 00/2041,803
CURRENT FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOSTWARE: Patentin Ver. 2.1
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Sequence 10944, Ap
Sequence 1131, Ap
Sequence 21402, A
Sequence 21402, A
Sequence 134, Ap
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 21, Appl
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100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION:
US-09-902-540-12184
US-09-949-0116-7806
US-09-949-016-7806
US-09-949-018-7806
US-09-824-574-7
US-09-248-796A-21359
US-09-248-796A-21402
US-09-248-796A-21402
US-09-002-540-14618
US-09-902-540-14618
US-09-902-540-14618
US-09-902-540-14618
US-09-902-540-14618
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US-09-902-540-14618
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US-08-960-022-6
US-09-565-808-2
US-08-822-264-3
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APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Takahashi, Tomoniro
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 6348334io
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
TITLE OF INVENTION: Encoding the Same
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. BOX 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi,
APPLICANT: Suda, Takashi,
Tomoniro
APPLICANT: Nakamashi, Tomoniro
APPLICANT: Nakamashi, Tomoniro
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
TITLE OF INVENTION: Encoding the Same
NUMBER OF SUGURNES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Blrch, Stewart, Kolasch & Birch
STREET: V.O. Box 747
CITY: Falls Church
STREET: Virginia
COUNTRY: USA
ZIP: 22040-0747
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TIRE: FLOWLY LIER:
COMPUTER: IBM PC compatible
DERAITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIPICATION: 45
ATTORNEY FACENT INFORMATION:
NAME: Murphy Ur., Gerald M.
REGISTRATION NUMBER: 110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8000
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LEUNGTH: 278 amino acids
murp. amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/339,214
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OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 26, Application US/08339214
; Patent No. 6348334
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Best Local Similarity 10v.
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; MOLECULE TYPE: protein
US-08-339-214-16
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclein acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FAPPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54959
LENGTH: 147
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43029
LENGTH: 452
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                                                                   Query Match
100.0%; Score 42; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative ,0; Mismatches 0; Indels
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100.0%; Pred. No. 28;
tive 0; Mismatches 0; Indels
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Pred. No. 3e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                US-09-270-767-54959
; Sequence 54959, Application US/09270767
; Patent No. 6703491
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; ORGANISM: Drosophila melanogaster
US-09-270-767-39742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Drosophila melanogaster US-09-270-767-54959
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 100.

Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6, Conservative
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287 IQPPLP 293
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US-09-270-767-43029
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US-08-339-214-16
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US/08/339,214

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180 QPPPLP 185
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                                                                                                                                                                                                                                                                                                              Length 278;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INC. 023712)
GENERAL INC. 023712)
GENERAL INCORMATION:
APPLICANT: YU, Guo-Liang
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Tumor Necrosis Factor Gamma
FILE REFERENCE: PF1413
CURRENT APPLICATION NUMBER: US/09/131,237C
CURRENT FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR PLICATION NUMBER: 09/005,020
PRIOR APPLICATION NUMBER: 09/461,246
PRIOR PLILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: 1998-06-05
PRIOR PRICING DATE: 1998-11-07
NUMBER OF SEQ ID NOS: 24
SOFFWARE: PATCHIL VET: 2.0
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APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Noten, Craig A.
TITLE OF INVENTION: Tumor Necrosis Factor Gamma
FILE REFERENCE: PF141P4
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                1110-139P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/09131237C; Patent No. 6599719
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FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULPIN Jr., Gerald M.
REGISTRATION NUMBER: 28,977
RREPENCE/DOCKET NUMBER: 111C
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8050
                                                                                                                                            TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-339-214-26
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US-09-246-129B-6
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GENERAL INPOGNATION:
GENERAL INPOGNATION:
GENERAL INPOGNATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196-0.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
IENGTH: 296
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270, 767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43189
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88.1%; Score 37; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/246,129B;
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 60/074,047
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 09/131,237
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-09
PRIOR FILING DATE: 1998-01-09
PRIOR FILING DATE: 1998-01-09
PRIOR FILING DATE: 1998-01-09
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
SOFTWARE: PAPLICATION NUMBER: PCT/US94/12880
PRIOR FILING DATE: 1994-11-07
SOFTWARE: PATENTING DATE: 1994-11-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-246-129B-6
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Best Local Similarity 100.
Matches 6; Conservative
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Sequence 32104, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32104

LENGTH: 642
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Patent No. 675314

GENERAL INPORMATION:

APPLICANT: Gioc, Loic

APPLICANT: Gioc, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 1090-03-19

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CLEAPALSEEPFORMATHER VERBION 0.9

SEQ ID NO 1357
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                     0; Indels

; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number Q16643
US-09-538-092-1357

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                     Mismatches
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32104
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Best Local Similarity 100.C
Matches 6; Conservative
                   6; Conservative
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                             294 QPPPLP 299
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                                                                    2 OPPPLP 7
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US-09-252-991A-32104
                Matches
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US-09-248-796A-18765
Sequence 18765, Application US/09248796A
Sequence 18765, Application US/09248796A
Sequence 18765, Application US/09248796A
Sequence 18765, Application US/09248796A
GENERAL INFORMATION: WOLZEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TILLE REPERENCE: 107196.132
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18765
LENGTH: 573
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1. LOCATION: (571)

1. THER INFORMATION: Identity of amino acid sequences at the above locations are unknd

US-09-248-796A-18765
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31536 Application US/09252991A

Patent No. 6551795

Batent No. 655176

Batent No. 655176

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31536
                                                                                                                                                                                                ö
                                                                                                                                            Length 313;
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88.1%; Score 37; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                          0; Indels
                                                                                                                                   88.1%; Score 37; DB 4; Lr
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
; LENGTH: 313
; TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-09-270-767-43189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                           Query Match
Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                          223 QPPPLP 228
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Best Local Similarity
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RESULT 15
US-08-718-661-2

Sequence 2, Application US/08718661

Patent No. 5876972

GENERAL INFORMATION:

TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation

TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation

TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation

NUMBER OF SEQUENCES: 15

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-085/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURSIFICATION NUMBER: US/08/718,661

FILING DATE:

CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 667 amino acids

TOPPOLOGY: linear

MOLECULE TYPE: protein

US-08-718-661-2
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527 QPPPLP 532
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Search completed: April 12, 2005, 08:07:48 Job time : 9.20909 secs

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Best Local S
Matches 7
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Sequence 1, Appli
Sequence 147458,
Sequence 37187, A
Sequence 175374,
Sequence 175374,
Sequence 17539, A
Sequence 17539, A
Sequence 148127,
Sequence 148127,
Sequence 148127,
Sequence 148127,
Sequence 14318,
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107.096 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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7 US-10-691-330-1

10-0424-599-147458

US-10-437-963-143948

US-10-437-963-175374

US-10-437-963-175374

US-10-369-493-9267

US-10-369-493-9267

US-10-369-493-9267

US-10-369-493-9267

US-10-424-599-148127

US-10-408-7565-2896

US-10-408-459-147426

US-10-437-963-143219
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Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length D
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Sequence 145289,
Sequence 190127,
Sequence 180130,
Sequence 137655,
Sequence 122529,
Sequence 122529,
Sequence 124132,
Sequence 192818,
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Sequence 264209,
Sequence 264209,
Sequence 264209,
Sequence 270730,
Sequence 270730,
Sequence 11116,
Sequence 131050,
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Sequence 177968,
Sequence 159895,
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US-09-899-495-68
US-10-2813-475-109
US-10-424-599-193704
US-10-424-599-193704
US-10-424-599-193704
US-10-437-963-17069
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US-10-437-963-130977
US-10-437-963-130977
US-10-437-963-130977
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Sequence 1, Application US/10281652;
Publication No. US2030091606A1
GENERAL INFORMATION:
APPLICANT: BUGHES, Thomas K.
APPLICANT: BOLDGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: UNABLOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
GURRENT APPLICATION NUMBER: US/09/641,803
FRIOR APPLICATION NUMBER: US/09/641,803
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR APPLICATION NUMBER: 60/149,310
SPRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE PATENTIN OF SEQ ID NOS: 34
SEQ ID NO I LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape.
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ORGANISM: Artificial Sequence
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MARINEAL INTERCALLICANT: REALLY, BARTON G.

APPLICANT: RAIL, BARTON G.

APPLICANT: RAIL, BARTON G.

APPLICANT: RAIL, BARTON G.

TITLE OF THYMENTON: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF THYMENTON: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF THYMENTON: HOWEN GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF THYMENTON: WORDER: US 00/100-2.3

FILING DATE: ABOUNDER: US 00/100-2.3

FROM RAILLY CATTON NUMBER: US 00/200-3.4

FROM RAILLY CATTON NUMBER: US 00/200-3.4

FROM RAILLY CATTON NUMBER: US 00/300-3.4

FROM
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N: EXPRESSED IN HEART, SIGNAL = 1.8

N: EXPRESSED IN BOLT LIVER, SIGNAL = 1.7

N: EXPRESSED IN BOAIN, SIGNAL = 2.7

N: EXPRESSED IN BOACENTA, SIGNAL = 2.7

N: EXPRESSED IN PLACENTA, SIGNAL = 2.7

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN BT474, SIGNAL = 2.7

N: EXPRESSED IN LIVEY, SIGNAL = 3.3

N: EXPRESSED IN LIVEY, SIGNAL = 3.3

N: EXPRESSED IN LIVER, SIGNAL = 3.3

N: EXPRESSED IN LIVER, SIGNAL = 3.3

N: EXPRESSED IN LIVER, SIGNAL = 3.3
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FEATURE:
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Best Local Similarity
Matches 6; Conserva
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OTHER INFORMATION:
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                                                           Sequence 1, Application US/10691330
| Publication Vo. US20050042300A1
| Publication No. US20050042300A1
| Publication No. US20050042300A1
| Publication No. US20050042300A1
| APPLICANT: Boldogh, Istvan
| APPLICANT: Boldogh, Istvan
| APPLICANT: Hughes, Thomas K., Jr.
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAWAGE
| TITLE OF INVENTION: UNBER: US/10/691,330
| CURRENT FILING DATE: 2003-10-22
| CURRENT PILING DATE: 2003-10-22
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: Patentin version 3.2
| LENGTH: 7
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Publication No. US20040031072A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON UNDER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147458
LENGTH: 76
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Query Match

Best Local Similarity 100.0%; Pred. No. 1.38+06;

Matches 7; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_104173C.1.pep
US-10-424-599-147458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Peptides US-10-691-330-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 37187, Application US/09864761; Patent No. US20020048763A1
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial
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19 LQPPPLP 25
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                                       US-10-691-330-1
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Sequence 9267, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gladman, Barry S.

APPLICANT: Gladman, Barry S.

TITLE OF INVENTION: BARRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: US/10/369, 493

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 9267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PELLON NUMBER: US/10/369, 493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
EBOTH: 572
LENGTH: 572
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Pred. No. 1.3e+03;
1; Mismatches 0; Indels
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92.9%; Score 39; DB 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 0
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Sequence 9495, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity 85.7%;
Matches, 6; Conservative
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9495
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US-10-369-493-9267
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105 LQPPPLP 111
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                     1 MOPPPLP 7
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                                                                                                                                                             JS-10-369-493-9267
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APPLICANT: La Rosa, Thomas J.
APPLICANT: A Rovalic, David K.
APPLICANT: Zou, Yihua
APPLICANT: Tou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 175374
LENGTH: 407
                                                                                              Sequence 143948, Application US/10437963
; Sequence 143948, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NO 143348
; LEUR MATTAN APPLICATION NUMBER: US/10/437,963
; SEQ ID NO 143348
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Pred. No. 9.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.9%; Score 39; DB 16; Length 332;
85.7%; Pred. No. 8.2e+02;
iive 1; Mismatches 0; Indels
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OTHER INFORMATION: Clone ID: PAT_MRT4530_73225C.1.pep

US-10-437-963-175374
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US-10-437-963-143948
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LOCATION: (1)..(407)
OTHER INFORMATION: unsure at all Xaa locations
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
116 LQPPPLP 122
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85 LQPPLLP 91
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                                                                                         US-10-437-963-143948
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APPLICANT: LE ROSA Thomas J
APPLICANT: LE ROSA Thomas J
APPLICANT: EN CONTIC David K
APPLICANT: Thou Yihua
APPLICANT: Thou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)8
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
EBO ID NO 147426
LENGTH: 414
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                                                           APPLICANT: Zhang, Bing

APPLICANT: Shang, Bing

APPLICANT: Glason, Bradford W.

APPLICANT: Glann, Gary W.

APPLICANT: Glann, Gary W.

APPLICANT: Warnock, Dalle B.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFERENCE: 660088 465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 256
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Pred. No. 8.8e+02;
1; Mismatches 0; Indels
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US-10-424-599-147426
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Pred. No. 1.4e+03;
1; Mismatches 0
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Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 147426, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 85.7%;
Matches 6; Conservative
                     Soumitra S.
Eoin D.
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Best Local Similarity 85.7;
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-10-408-765A-2896
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ORGANISM: Glycine max
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JS-10-424-599-147426
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US-10-437-963-143219
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US-10-369-493-17539

is Sequence 17539, Application US/10369493

sequence 17539, Application No. US20030233675A1

igeneral INFORMATION:

APPLICANT: Goo, Yongweir

APPLICANT: Good Good Barry S.

APPLICANT: Good Good Barry S.

APPLICANT: Chen, Xianfeng

ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EPANTS WITH IMPROVED PROPERTIES

ITILE OF INVENTION: ENANTS WITH IMPROVED PROPERTIES

ITILE OF INVENTION: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

WUMBER OF SEQ ID NOS: 47374

LENGTH: 612
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENITION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENITION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 148127
LENGTH: 189
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Pred. No. 1.4e+03;
1; Mismatches 0; Indels
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Pred. No. 6.7e+02;
1; Mismatches 0; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_104780C.1.pep
US-10-424-599-148127
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LOCATION: (1)..(189)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 85.7%;
Matches 6; Conservative
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; ORGANISM: Xylella fastidiosa
US-10-369-493-17539
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 LQPPPLP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 MKPPPLP 111
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; Sequence 2896, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION:

RESULT 11 US-10-408-765A-2896

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Length 38;

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88.1%; Score 37; DB 10; I
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
   APPLICANT: Wang, Jun
APPLICANT: Liu, Derong
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00069U31
CURRENT FILING DATE: 2001-03-09
FRIOR APPLICATION NUMBER: 60/188,517
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn version 3.0
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 12, 2005, 07:55:20 Job time : 22.7 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Homo sapiens
US-09-802-668-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 QPPPLP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OPPPLP 7
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 142219
LENGTH: 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%; Score 38; DB 16; Length 812; 85.7%; Pred. No. 2.5e+03; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44149C.1.pep
US-10-437-963-143219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.1%; Score 37; DB 10; I 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERKEAL INFORMATION:
APPLICANT: Renjamin, Christopher W. APPLICANT: Rainowsky, Alla M. APPLICANT: Rainowsky, Alla M. APPLICANT: Rainowsky, Alla M. APPLICANT: Rainowsky, Alla M. ITILE OF INVENTION: Human Ion Channels FILE REPERENCE: 001880U51
CURRENT APPLICATION NUMBER: 06/215,815
PRIOR APPLICATION NUMBER: 60/216,481
PRIOR APPLICATION NUMBER: 60/216,481
PRIOR PILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-06
PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 68, Application US/09899495; Publication No. US20030088060A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wood, Linda
APPLICANT: Vogeli, Gabriel
APPLICANT: Karnovsky, Alla
APPLICANT: Linske-O'Connel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
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US-09-899-495-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||||||
26 VQPPPLP 32
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25 QPPPLP 30
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 12, 2005, 07:49:31 ; Search time 5.02727 Seconds (without alignments) 133.973 Million cell updates/sec Run on:

US-10-691-330-1 42 1 MQPPPLP 7 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	arco	Query	Query Match Length	g	Ę	Description
:	21000	וומרכזו	TO STORY	3 !		
-	40	95.2	1776	7	G86280	protein T5E21.13 [
7	39	92.9		~	E82756	beta-galactosidase
m	38	90.5		~	T02441	DNA- (apurinic or a
4	38	90.5	542	N	н86239	protein P20B24.8 [
S	37	88.1	164	~	T15525	hypothetical prote
9		88.1	178	7	T00644	
7	37	88.1	186	7	T22685	
σ,	37	88.1	211	7	S55129	G
6	37	88.1	278	~	A49266	fas ligand - rat
10	37	88.1	393	7	T00575	probable WRKY-type
11	37	88.1	471	8	T21349	hypothetical prote
12	37	88.1	483	~	A25896	beta-adrenergic re
13	37	88.1	588	~	E96633	probable Serine/Th
14	37	88.1	620	~	S06733	hydroxyproline-ric
15	37	88.1	649	~	5080NC	drebrin E (clone g
16	37	88.1	651	~	T14763	hypothetical prote
17	37	88.1	731	~	JC7701	ARHGAP9 protein -
18	37	88.1	749	~	G86186	hypothetical prote
19	37	88.1	830	~	T18860	hypothetical prote
20	37	88.1	1124	7	JX0293	Ω
21	37	88.1	1125	~	T19193	hypothetical prote
22	37	88.1	1154	7	A56242	E-box-binding repr
23	37	88.1	1291	~	T17242	hypothetical prote
24	37	88.1	136	7	T00250	MEGF2 protein - hu
25	37	88.1	1560	~	T00080	hypothetical prote
56	36	85.7	48	~	S23410	FUN19 protein - ye
27	36		505	~	S72273	actin-depolymerizi
28	36	85.7	4	~	JC7391	Ca2+-binding prote
53	36	85.7	610	~	T22687	hypothetical prote

dishevelled homolo	hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote	F14L17.21 protein	protein F1K23.14 [hypothetical prote	protein F23F12.6 [hypothetical prote	hypothetical prote	hypothetical prote	CW17R protein - mo	hypothetical prote	probable transcrip	transcription fact
151691	T49835	A36378	T47307	T25119	A86279	G86411	F96507	A88485	T47365	T21481	T19550	S52735	S49942	S72468	G02919
7	7	~	~	~	7	~	7	~	~	7	~	7	0	~	7
736	795	823	267	300	312	321	337	414	426	486	494	548	587	597	639
85.7	85.7	85.7	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3
36	36	36	35	35	35	32	32	35	32	35	35	35	32	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Greeces: Arabidopsis thaliana (Greecest Cress)
C;Species: Arabidopsis thaliana (Greecest Cress)
C;Species: Arabidopsis thaliana (Greecest Cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86280
C;Accession: G86280
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jeni, X.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C., J.J.; J.J.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Ttele: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G86280
A;Accession: G86280
A;Accession: G86280
A;Residues: 1-1776 <STOONA
A;Residues: 1-1776

A;Residues: 1-1776 <STO> A;Cross-references: UNIPROT:Q9MA20; GB:AE005172; NID:g7527720; PIDN:AAF63169.1; GSPDB:GN C;Genetics

A, Map position: 1

Gapa ö Length 1776; Score 40; DB 2; Length 17.7. Pred. No. 2.1e+02; 1; Mismatches 95.2%; 85.7%;

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|||||:| 1643 MQPPPMP 1649 7 1 MOPPPLP 엄

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RESULT 2

beta-galactosidase XF0840 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: 882756 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MuID:20365717; Pathogen Xylella fastidiosa. A;Note: for a complete list of authors see reference number A59328 below

A;Status: preliminary A; Accession: E82756

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A;Molecule type: DNA A;Reaidues: 1-612 <SIM> A;Cross-references: UNIPROT:Q9PF38; GB:AE003923; GB:AE003849; NID:g9105736; PIDN:AAF8365 A;Experimental source: strain 9a5c

a

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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86239
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Anture 408, 816-820, 200
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Roney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Sinin, P.; Southwick, A.M.; Sun, H.; Tallon, J. A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-542 <STO>
A,Cross.references: UNIPROT:Q9SGY5; GB:AE005172; NID:g6573750; PIDN:AAF17670.1; GSPDB:GN(
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C, Jacession: T00644

R; Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
i Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
A; Reference number: Z14197
A; Reference number: Z14197
A; Accession: T00644
A; Accession: T00644
A; Accession: Tpo644
A; Recule type: DNA
A; Residues: 1-178 < FED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pypothetical protein C16B8.3 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CjAccesion: T1525
RjBentley, D.
AjBentley, D.
AjBentley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F316.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2; Length 542
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 VÕPPPLP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OPPPLP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:C16B8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: F20B24.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm O.D.; Junqualiza, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr A;Authors: Martins, A.M.; Madens, M.V.; Martins, E.M.F.; Matsukumai, A.Y.; Marion, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukumai, A.Y.; Marno, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukumai, A.Y.; Mannok, C.F.M.; Miraca, E.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, A.Y.; Mannok, C.F.M.; Miraca, E.C.; Palmieri, D.A.; Anthors: da Silva, A.C.R.; da Silva, A.M.; Salva Jr., W.A.; da Silva; A.M.; Salva Jr., W.A.; da Silva; A.M.; Silva Jr., W.A.; da Silvai, A.M.; Silva Jr., S
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85.7%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Pred. No. 99;
1; Mismatches
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C,Superfamily: beta-galactosidase bga
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1 MOPPPLP 7

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Local Similarity 85.7

Best Loca Matches

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356 LQPPPLP 362

1 MOPPPLP 7

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C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
R=11 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor A;Reference number: A49266; MUID:94084792; PMID:7505205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: A49266
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-278 - SUD>
A,Cross-references: UNIPROT: P36940, GB: U03470; NID: g440178; PIDN: AAC52129.1; PID: g440179
C,Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable WRKY-type DNA binding protein [imported] - Arabidopsis thaliana
NiAlternate names: probable DNA-binding protein T2/E13.1
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Decies Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00575; B84706
C;Accession: T00575; B84706
S;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
A;Reference number: Z14178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Accession: T00575
A.Status: translated from GB/EMBL/DDBJ
A.Status: D.33 «ROUS
A.Cross-references: UNIPROT:022921; EMBL:AC004165; NID:g3150396; PID:g3150397
A.Experimental source: cultivar Columbia
R.Inin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
asture, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Accession: B84706
A.Accession: B84706
A.Accession: By Town A.Accession: Bayon A.Acce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                          Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 278
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                          DB 2;
66;
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88;
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                                          Query Match 88.1%; Score 37; Best Local Similarity 100.0%; Pred. No. Matches 6; Conservative 0; Mismatc
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Best Local Similarity 100.
Matches 6; Conservative
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A,Map position: 2
                                                                                                                                                                                                                                                                                                                                            154 QPPPLP 159
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A;Reference number: $17249; MUID:92020118; PMID:1923755
A;Accession: $17249
A;Accession: $17249
A;Residues: 1-113.'V'.115-211 <EST>
A;Residues: 1-113.'V'.115-211 <EST>
A;Cross-references: EMBL:X59861; NID:g4317; PIDN:CAA42521.1; PID:g4318
C;Genetics:
A;Gene: SGD:RGM1
A;AGNOST-References: SGD:S0004794; MIPS:YMR182C
A;Map position: 13R
C;Keywords: DNA binding; transcription factor; zinc finger
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A;Experimental source: clone F55A11
A;Cross-references: UNIPROT:048681; EMBL:AC002396; NID:g2749918; PID:g2829866; GSPDB:GNC
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A;Residues: 1-211 <CHU>
A;Cross-references: UNIPROT:000453; EMBL:249808; NID:g854440; PID:g854452; MIPS:YMR182c
A;Experimental source: strain AB972
R;Estruch, F.
Nucleic Acids Res. 19, 4873-4877, 1991
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22685
S;Kershaw, J.
Submitted to the EMBL Data Library, May 1996
A;Reference number: Z19600
A;Accession: T22685
A;Accession: T22685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-186 <WILL>
A;Acstatus: 1-186
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N;Alternate names: protein YM8010.12c; protein YMR182c
C;Species: Saccharomyces cerevisiae
C;Date: Objul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S55129; S17249
R;Churcher, C.M.
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                                                                                    A;Gene: ATSP:F316.7
A;Map position: 1
A;Introns: 50/3; 87/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F316.7
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58;
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hypothetical protein F55A11.1 - Caenorhabditis elegans
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Best Local Similarity 100.
Matches 6; Conservative
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A,Gene: CESP:F55A11.1
A,Map position: 5
A,Introns: 33/3; 59/2; 146/2
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162 QPPPLP 167
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Marziali, Romey, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: E96633
A; Accession: E96633
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-588 <STO>
A; Cross-references: UNIPROT: 022717; GB: AE005173; NID: 92462749; PIDN: AAB71968.1, GSPDB: GNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxyproline-rich glycoprotein precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Reb-1990 #sequence_revision 28-Reb-1990 #text_change 09-Jul-2004
C;Accession: 306733
R;Keller, B.; Lamb, C.J.
R;Keller, B.; Lamb, C.J.
A;Title: Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene : A;Reference number: 806733; WUID:90128263; PMID:2612909
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R;Toda, M.; Shirao, T.; Minoshima, S.; Shimizu, N.; Toya, S.; Uyemura, K.
Biochem. Biophys. Res. Commun. 196, 468-472, 1993
A;Title: Molecular cloning of cDNA encoding human drebrin E and chromosomal mapping of i.
A;Reference number: JN8809; MUID:94030036; PMID:8216329
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A,Residues: 1-649 <TOD>
A;Cross-references: UNIPROT:Q16643; DDBJ:D17530; NID:g498650; PIDN:BAA04480.1; PID:g4986:
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Residues: 1-620 <KEL>
A, Residues: 1-620 <KEL>
A, A, Cross-references: UNIPROT: P13983; EMBL: X13885; NID: 919866; PIDN: CAA32090.1; PID: 919867
C, Superfamily: hydroxyproline-rich glycoprotein
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drebrin E (clone gDbh13) - human
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.1%; Score 37; DB 2; Length 620; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           88.1%; Score 37; DB 2; L
100.0%; Pred. No. 1.9e+02;
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.1
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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C; Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 QPPPLP 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 QPPPLP 430
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                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                      A; Gene: F8A5.31
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                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z19411
A;Reference number: Z19411
A;Accession: T21349
A;Residues: 1.471 < WIL>
A;Residues: 1.471 < WIL>
A;Residues: 1.471 < WIL>
A;Cross-references: UNIPROT: Q93571; EMBL: Z79754; PIDN: CAB02096.1; GSPDB: GN00019; CESP: F2
A;Cross-references: UNIPROT: Q93571; EMBL: Z79754; PIDN: CAB02096.1; GSPDB: GN00019; CESP: F2
C;Genetics:
A;Gene: CESP: F2542.8
A;Gene: CESP: F2542.8
A;Introns: 26/3; 138/3; 302/3; 353/3; 379/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F25H2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A25896

beta-adrenergic receptor - turkey

beta-adrenergic receptor - turkey

C;Species: Melagaris gallopavo (common turkey)
C;Species: Melagaris gallopavo (common topacies)
C;Sacession: A25896
A;Title: The avian beta-adrenergic receptor: primary structure and membrane topology.
A;Reference number: A25896
A;Molecule type: mRNA
A;Residues: 1-483 xARP.
A;Residues: 1-483 xARP.
A;Residues: Usuria sayaria (B:M14379; NID:g213891; PIDN:AAA49627.1; PID:g213892
A;Experimental source: erythrocyte
C;Superfamily: vertebrate rhodopain
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                   ypothetical protein F25H2.8 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Material T21349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 471;
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                                                                                                                                                                                                                                                                                                         R;Wilkinson, J. submitted to the EMBL Data Library, September 1996
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Query Match
Best Local Similarity 71.4
Matches 5; Conservative

:||||:| 451 LOPPPIP 457

1 MOPPPLP 7

ò 유 Query Match 88.1 Best Local Similarity 100. Matches 6; Conservative

|||||||| QPPPLP 261

g 8

RESULT 13 E96633

2 QPPPLP 7

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2 QPPPLP 7 |||||| 363 QPPPLP 368

Search completed: April 12, 2005, 07:56:46 Job time : 7.02727 secs

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Acres 1

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 12, 2005, 07:49:31; Search time 33.2182 Seconds (without alignments) 107.909 Million cell updates/sec

US-10-691-330-1 42 1 MQPPPLP 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

+[tipod		*			SUMMAKIES	
No.	Score	Match	,c	DB		Description
-	42	100.0	1		Q9VAXS	
7	40	95.2	600	7	Q8GPV8	
e	40	95.2	785	7	Q8RXF1	
4	40	95.2	1776	~	Q9MA20	
ß	39	92.9	218	7	Q6C180	
9	39	92.9	222	-	COLI THUOB	
7	39	92.9	315	~	Q75AM7	ashbya
00	39	92.9	612	7	Q87AJ2	Q87aj2 xylella fas
6	39	92.9	612	7	Q9PF38	
10	39	92.9	701	-4	CG1 HUMAN	
11	39	92.9	1074	Н	EMIZ MOUSE	
12	39	92.9	1395	~	Q7SC01	
13	39	92.9	1404	7	Q9GRR6	
14	38	90.5	199	N	Q7QRU8	Q7gru8 giardia lam
15	38	90.5	256	~	Q6Z074	
16	38	90.5	536	Н	ARP_ARATH	
17	38	90.5	542	~	Q9SGY5	
18	38	90.5	678	~	Q8TES7	homo a
19	38	90.5	812	0	Q8LIE4	
20	38	90.5	2165	~	Q8MMX0	
21	38	90.5	2879	N	Q6LFQ9	
	37	88.1	44	N	Q85G37	cyanid
23	37	88.1	68	~	Q6QZQ3	
	37	88.1	72	~	Q87610	
25	37	88.1	73	7	Q87603	
56	37	88.1	66	7	Q87482	Q87482 chimpanzee
27	37	88.1	114	~	060202	
28	37	88.1	126	۲۹	Q9NDS2	penaeus
53	37	88.1	126	~	Q9NDS3	penaeus
30	37	88.1	128	~	Q8GYP2	/p2 arabidop
31	37	88.1	134	7	Q74ZR7	
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Q84QQO oryza sativ Q18043 caenorhabdi O76192 galleria me O48681 arabidopsis Q6983 oryza sativ Q20796 caenorhabdi Q811b5 mus musculu Q62st9 homo sapien Q0453 saccharomyc Q8p6x9 xanthomonas	Q7xdt9 oryza sativ Q6yzu3 oryza sativ Q6zbh3 oryza sativ
0840Q0 018043 SERO GALME 04681 020796 021796 091185 0625T9 0825T9 0885X9	Q7XDT9 Q6YZU3 Q6ZBH3
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137 164 164 178 178 196 190 201 223	226 233 233
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	88.1 88.1 88.1
	37
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2 018043 0 0	T 1 Sylvax5 PRELIMINARY; PRT; 261 AA. GOYAX5; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-OAT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) CG12872-PA. CG12872-PA. CGRPNames=CG12872; Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Roepterar; Endopterygoteryjota; Dipterar, Brachycera; Muscomorpha; Rohydraidea: Drosophiladea: Drosophila brosophila.	NCBLTAXID=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RN [1] RN DIGINUSE FROM N.A. Addams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addams W.D., Celniker S.E., Holt R.A., Zhang Q., Chen L.X., R. Baracis S.E., Richards S.A., Ashburner M., Henderson S.N., Sutton G.G., Wortens J.R., Yandell M.D., Zhang Q., Chen L.X., R. Baracis S.E., Richards S.C., Champe M., Ffeiffer B.D., Rank M., Basul A., Baracis R.G., Champe M., Ffeiffer B.D., Rank M., Basul A., Baxendale J., Bayraktergolu L. Besaley E.M., Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., R. Bockova D., Botchan M.R., Bouck J., Brckstein P., Brottier B., Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., R. Cherty J.M., Cawley S., Dahlke C., Perreite S., Center A., Chandra I., R. Burtis K.C., Busam D.A., Butler H., Codleu E., Center A., Changer C., Perreite S., Plaischmann W., R. Bouck J., Bernale J., Bouck J., Bernale S., Plaischmann W., R. Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Houston K.J., Bavangelista C.C., Perreitez C., Perreites S., Plaischmann C., Adalain F., Kadrey D., Heinand T.J., Wei M.H., Ibegwam C., A., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., A., Houston K.A., Howland T.J., Wei M.H., Nalus D., Lai Z., Liang Y., Lin X., Houston K.A., Houston K.A., Howland T.J., Wei M.H., Nalus D., Lai Z., Liang Y., Lin X., Mattel B. McIntosh F., Karper G.H., Keal, Kennison J., Moshreti A., Mattel B. McIntosh W., Murphy B., Murphy D., Morris J., Moshreti A., Mattel B., McIntosh W., Murphy B., Murphy D., Morris J., Moshreti A., Mattel B., Kalpen K.A., Mixon K., Weinsen D., Parlarion M., Pittman G.S., Pan S., Pollard J., Purla S., Palaling A., Sulder Kamos I., Simpson M., Stupeki M., Weinsen B.C., Siden Kamos I., Simpson M., Stupeki M., Wang R.W., Wang F.W., Wang S., Wang S., Wang S., W
11 184 11 186 11 186 11 186 11 223 11 223 11 223	PRELIMINARY, (TrEMBLrel. 1 (TrEMBLrel. 2 (TrEMBLrel. 2 1872 1	PERON N.A. Celniker S.E. Celniker S.E. G., Scherer Y.H. C., Rogers Y.H. C., Rogers Y.H. Doyle C., Baxte Doyle C., Baxte C., Basu A., Bax M., Basu A., Bax W., Basu A., Bax W., Cawley S., Dowly L.E., Corre L., Harvey D., Stradling A.C., Stradling F.N., Zavong F.N., Zavong F.N., R. Zbong F.N., R. Zbong F.N., R.
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	T 1 5 6 909AX5 909VAX5 01-MAY-2000 (TrE) 01-MAY-2003 (TrE) 01-MRR-2003 (TrE) 0212872-PA. 08FNAMMS=CG12872 Drosophila melanz Eukaryota, Metaz. Bukaryota, Metaz. Bukaryota, Eukazyota, Eukaz	Taxides; June Project of the Project
, , , , , , , , , , , , , , , , , , ,	RESULT 1 Q9VAX5 ID Q9VAX5 DT Q9VAX5; DT 01-MAY: DF 01-BAY: DE CG12872 GN ORFWAME OC BUKATYON OC RUKATYON	OCC SUBJUST ON COLUMN TO SURE THE SECTION OF SUREDILING THE SUREDI

Science 287:2185-2195(2000)

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DOI=10.1128/JB.184.23.6665-6680.2002;
Larbig K.D., Christmann A., Johann A., Klockgether J., Hartsch T.,
Merkl R., Wiehlmann L., Fritz H.J., Tummler B.;
Merkl R., Wiehlmann L., Fritz H.J., Tummler B.;
Mene islands integrated into IRNA(Gly) genes confer genome diversity
on a Pseudomonas aeruginosa clone.";
J. Bacteriol. 184:6665-6680(2002).
EMBL, ARA40524; AAN62266.1; -..
REMBL, ARA40524; AAN62266.1; -..
REMBL, ARA40524; AAN62266.1; -..
RICEPPO: IPRO11093; DUF1528.
RICEPPO: IPRO1119; Relax Tral.
R Fam; PF07515; DUF1528; 1.
R Fam; PF07514; Tral.2; 1.
R SWART; SMO0471; HDG; 1.
Hypothetical procein.
W Hypothetical procein.
W SEQUENCE 600 AA; 66371 MW; BF43COAOE10FFF9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Nguyen M., Karlin-Veumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Veumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Boweer L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narursaka M., Pham P.K., Sakano H.,

Sakurai T., Satcu M., Saki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.,

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

HSSP, Q862M4, 1AAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 40; DB 2; Length 600;
85.7%; Pred. No. 5.5e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.2%; Score 40; DB 2; Length 785; 85.7%; Pred. No. 7.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMOGD13, UBQ; 1.
PROSITE; PS50128; SURP; 2.
PROSITE; PS50128; SURP; 2.
PROSITE; PS50053; UBIQUITIN 2; 1.
SROUENCE 785 AA; 87536 MW; A1958C193E63BDC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UTN-2002 (TrEMBLrel. 21, Created).
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Splicing factor, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              785 AA.
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Arabidopsis thaliana (Mouse-ear cress).
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GO; GO:0066396; P:RNA processing; IEA.
InterPro; IPR000661; Surp.
InterPro; IPR00626; Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01805; Surp; 2.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.7
nes 6; Conservative
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QBRXF1
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                                                                                                MEDLINE-212426665; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Tardecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettemoourt B.R., Celniker S.E., de Grey A.D., Dryedale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: a
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0039569; CG12872.
SEQUENCE 261 AA; 28401 MW; D5753D823160DAA6 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein ORF SG44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Best Local Similarity 100.
Matches 7; Conservative
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194 MQPPPLP 200
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652 MQPPPMP 658 1 MQPPPLP 7 à

6; Conservative

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

Pseudomonas aeruginosa.

RESULT 2
08GPV8
1D 08GPV
AC 08GPV
DT 01-M
DT 0

Q8GPV8

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STRAIN=SG17M; MEDLINE=22313472; PubMed=12426355;

SEQUENCE FROM N.A. NCBI_TaxID=287

Gaps

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Q9MA20

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Mincker P., Souciet J.L.,
T. "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation (Pro-opiomelanocortin) (POMC)
(Contains: Corticotropin precursor (Pro-opiomelanocortin) (ACTH);
Melanotropin alpha (Alpha-MSH); Corticotropin-like intermediary
peptide (CLIP); Lipotropin beta (Reta-MSH); Beta-endorphin; Met-enkephalin].
Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
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Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG78391.1; -.
SEQUENCE 218 AA; 24159 MW; A859A029FB99BC4B CRC64;
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85.7%; Pred. No. 2.6e+02;
ive 1; Mismatches 0;
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5. Conservative
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TISSUE=Pituitary;
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                                                                                                             NCBI_TaxID=284591;
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                                                                                                                                                                               STRAIN-CLIB99;
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Tambunga G., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriuni M., Vaysberg M., Yu G., Federspiel N.A.,
Theologis A., Ecker J.R.,
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi B., Conn L.,
Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.
Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.
Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A
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PROSITE; PS50053; UBIQUITIN 2; 1.
SEOUENCE 1776 AA; 200270 MW; CIC28169934E0A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC010657; AAF63169.1; -.
FIR, G86280, G86280.
HSSP, Q662M4; IAR, binding; IEA.
GO; GO:000373; F:RNA binding; IEA.
GO; GO:000396; P:RNA processing; IEA.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                       PRT; 1776 AA
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Interpro; IPR000626; Ubiquitin.
Pfam; PF01805; Surp; 4.
Pfam; PF00240; ubiquitin; 1.
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                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
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SMART; SM00213; UBQ; 1.
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                       PRELIMINARY;
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06C180;
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Length 218; 0; Indels us-10-691-330-1.rup

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Query Match
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to the kuropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Melanotropin alpha.
Corticotropin alpha.
Corticotropin like intermediary peptide.
Lipotropin bera.
Lipotropin gamma.
Melanotropin beta.
Meta-endorphin.
Poly-Ser.
Poly-Ser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008917; Euk_transcr_DNA.
InterPro; IPR00827; TF_DIP.
Pfam; PF00170; bZIP.1; TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=ADL104W;
Ashbya gossypli, (Yeast) (Eremothecium gossypli).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Fremothecium.
                                                                                                EMBL, AB020971; BA335125.1; -.
InterPro. 1 BRA35125.1; -.
Fram, PR00976; ACTH domain, I.
PRINTS; PR00383; MELANOCORTIN.
ProDom; P003250; Mcortin ACTH, 1.
Cleavege on pair of basic residors, Endorphin; Hormone; Signal.
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Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.9%; Score 39; DB 2; Length 315; 85.7%; Pred. No. 3.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 222,
Pred. No. 2.78+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. -1- SMILARITY: Belongs to the bZIP family. EMBL, AEO16817. AASS1816.1; -AGD, ADL104W; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMAKKITE, PSCO217, BIZIP, 1.
PROSITE, PSCO017, BIZIP, 1.
PROSITE, PSCO0036, BZIP, BASIC, 1.
DNA-binding; Nuclear protein.
SEOUENCE 315 AA; 34594 MW; 27AED42A1046A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7868C713D6360B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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24970 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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107
107
222
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195
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222 AA;
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LQPPPLP 68
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Best Local Similarity
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Q75AM7
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MEDLINE=22421311; PubMed=12533478;
XX DOI=10.128/MB.185.3.1018-1026.2003;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Nayaki C.Y., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.H.,
A Takte M.A., Lemos B.G.M., Machado M.A., Ferro M.T.T. da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
Baia G.S., Blanco M.S., Cannavan F.S., Celestino A.V.,
A dc Cunha A.F., Ferille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
Leoni S.G., Oliveira A.R., Rosa W.E. Jr., Sasaki F.T., Sena J.A.D.,
A de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 185:1018-1026(2003).

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-aglactores residues in beta-D-galactosides.
-!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
EMBL, AE012560, AA029665.1; -- Gamily 35 of glycosyl hydrolases.
GO; GO:0003341; C:beta-galactosidase complex; IEA.
GO; GO:0016798; F:hydrolase activity, IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
InterPro; IPR009979; Gal bind like.
InterPro; IPR009974; Glyco-hydro-35.
PFam; PF01301; Glyco-hydro-35.
PFam; PF01301; Glyco-hydro-35.
PRINTS; PR013042; GLHYDRLASE35.
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                                                                                                                                                                                                                                                                                                                                                                Name-bga; OrderedLocusNames-PD1833;
Xylella fastidiosa (strain Temecula1 / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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"Comparative analyses of the complete genome sequences of I disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2; Length 612;
Pred. No. 7.8e+02;
1; Mismatches 0; Indels
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Complete protecome; Glycosidase; Hydrolase.
SEQUENCE 612 AA; 67992 MW; 2866663591EB556B CRC64;
                                                                                                                                                                                                                                     01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                   612 AA
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                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-galactosidase.
OrderedLocusNames=Xf0840;
Xylella fastidiosa.
                                                                                                                                                                                PRELIMINARY;
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101 LOPPELP 107
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                                                                                                                                                                                                                                                                                                                                 Beta-galactosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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08K482;
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                                                                                                                                                                               SIGNATURE=20365717; PubMed=10910347; DOI=10.1038/35018003;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barrose M.H., Bonacocrafi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colaubo C., Coosta P.F., Costa M.C.R., Coosta-Neco C.M., Colaubo C., Colombo C., Costa M.C.R., Coosta M.C.R., Coosta-Neco C.M., Coutinho L.L., Cristofani M. Dias-Prerbie W. Perro J.A., Rada G.H., Ferreira V.C.A., Ferro J.A., Rarda S.C., Franco M.C., Frohme M., Pullan L.R., Garnier M., Goldman G.H., Coldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Lemos B.G.M., Lopes S.A., Lopes C.R., Machado J.A., Madeira A.M.B.N., Madeira H.M.F., Marrino C.L., Marchado M.A., Madeira A.M.B.N., Matchins B.M.F., Marchins B.A., Martins M.V., Morto L.B.S., Monn D.H., Noberga F.G., Nunse L.R., Oliveira M.S., A de Oliveira M.C., de Oliveira M.C., de Oliveira H.A. Jr., Pesquero J.B., de Soluza A.A., de Silva A.R., da Silva A.R., da Silva R.C., Palmieri D.A., Paris A., da Silva A.C.R., da Silva A.C.R., da Silva R.R., Silva W.J., de Soluza A.A., Vallada H., Van Sluys M.A., Verjovski.Almeida S., Vettore A.L., The Sago M.A., Zatz M., Meidanis J., Setubal J.C.; Justucke 406.151-159 (2000).
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-! - SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
EMBL, AE003923; AAF83650.1; -.
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GO; GO:0004565; F:beta-galactosidase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR0018979; Gal_bind_like.
InterPro; IPR001894; Glyco_hydro_35.
Pfam; PF01301; Glyco_hydro_35; I.
PRINTS; PR00742; GLHYDRIASE35.
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name=CXorfé, Synonyne=CG1;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Complete protecome; Glycosidase; Hydrolase.
SEQUENCE 612 AA; 67893 MW; B894D6A3EB789BCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.9%; Score 39; DB 2; 1
85.7%; Pred. No. 7.8e+02;
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Best Local Similarity 85.7°
                                  Xanthomonadaceae; Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406:151-159(2000).
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356 LOPPPLP 362
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                                                                                                                                  SEQUENCE FROM N.A.
                                                             NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG1_HUMAN
Q13495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
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                                                  MEDLINE=96225444; PubMed=8640223; Laporte J., Kioschis P., Coy J., Laporte J., Hu L.-J., Kretz C., Mandel J.-L., Kioschis P., Coy J., Klauck S.M., Poutska A., Dahl N.; Agene mutated in X-linked myotubular myopathy defines a new putative tyrosine phosphatase family conserved in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITRE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collina F.S., Wangner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., McGwan N.J., McKernan K.J., Mallahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=C57BL/6J; TISSUE=Cochlea;
MEDLINE=22722101; PubMed=12837629; DOI=10.1016/S1044-7431(03)00075-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created) .
10-OCT-2003 (Rel. 42, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
25-JAN-2005 (Rel. 46, Last annotation update)
(Elastin microfibril interfacer 2) (Basilin).
                                                                                                                                                                                                                      Nat. Genet. 13:175-182(1996).
-!- TISSUE SPECIFICITY: Preferentially expressed in skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amma L.L., Goodyear R., Faris J.S., Jones I., Ng L., Richardson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rest D.;
emilin family extracellular matrix protein identified in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADICIBE4F6DFD34E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 1;
Pred. No. 9e+02;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1074 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poly-Pro.
Poly-Gln.
Poly-Gln.
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. Cell. Neurosci. 23:460-472(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74475 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U46023; AAC50551.1; -. Genew; HGNC:2568; CXorf6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.",
Best ac 6; Conservative
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429
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                            Dev. Biol. 249:204-218(2002).

-1- FUNCTION: May be responsible for anchoring smooth muscle cells to elastic fibers, and may be involved not only in the formation of the elastic fibers, and may be involved not only in the formation of the elastic fibers, and may be involved not only in the formation of the elastic fiber, but also in the processes that regulate vessel assembly. Has cell adhesive capacity. Major component of the cochlear basilar membrane (BM) which may contribute to the developmental assembly or function of the BM.

-1- SUBUNIT: Homotrimer associated through a moderately stable interaction of the triple heltx and then a further quaternary assembly to higher order polymers via intermolecular disulfide bunds (BV similarity). Interacts with EMILINI.

-1- SUBCELLULAR LOCATION: Extracellular matrix. Found mainly at the interface between amorphous elastin and microfibrils.

-1- SUBCELLULAR LOCATION: Extracellular matrix. Found mainly at the bunds followed by modest levels in adult heart and lung, and much lower levels in forebrain, brainstem, cereballum and hypothalamus.

-1- TISSUE SPECIFICITY: Highest levels are present in cochlea of PB pups, followed by modest levels in adult heart and lung, and much lower levels in forebrain, brainstem, cereballum and hypothalamus.

-1- DEVELOPMENTAL STAGE: Low levels detected in cochlea in neonatal pups at Pl: Levels increased 2-fold by P5 and rose further to 16-fold at Pl3: Expression declined somewhat in adult mice. At E9:5, as during all stagges of development, it is strongly expressed in citerathy and in the limbbuds and the heart.

-1- SIMILARITY: Contains 1 collagenous domain.

-1- SIMILARITY: Contains 1 collagenous domain.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Scheln J.E., Jones S.J.M., Marza M.A., Scheln J.E., Jones S.J.M., Marza M.A.
                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE.
MEDLINE=22209197; PubMed=12221002; DOI=10.1006/dbio.2002.0764;
Lefineister C., Steidl C., Schumacher N., Erhard S., Gessler M.;
"Developmental expression and biochemical characterization of Emu family members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clq.
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:2389156; Emilin2.
InterPro; IPR001073; Clq.
InterPro; IPR00893; TNF_like.
Pfam; PF00386; Clq; 1.
PROSITE; PS50871; Clq; 1.
Cell adhesion; Coiled coil; Collagen; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coiled coil (Potential).
                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro-rich.
Collagen-like.
Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
EMILIN 2.
EMI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF468645; AAM53532.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC053753; AAH53753.1; -.
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CARBOHYD
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A Galagan J. E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Jaffe D., Fitzudpi W., Man D.-Ö., Smirnov S., Purcell S., Rehman B.,
B. Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Dui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinney J.A., Braun B.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Netzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catchenide D., ii W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A raden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Natrig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
 (GlonAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Predicted protein (Hypotherical protein B22K18.130).
Name=NCU09482.1; Synonyms=B22K18.130;
Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                    Length 1074;
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                                                                                                                                                  Score 39; DB 1; Length 107
Pred. No. 1.4e+03;
1; Mismatches 0; Indels
                                                                                                                 MW; 4B81728C83CE52A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1395 AA; 149956 MW; CB0D84322CDA8835 CRC64;
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 N-linked
N-linked
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PROSITE; PS50014; BROMODOMAIN_2; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AABX01000145; EAA33970.1;
EMBL; BX842597; CAE75735.1; -.
463 463
514 514
586 586
615 615
744 744
995 995
1074 AA, 117310 M
                                                                                                                                                    92.98;
                                                                                                                                                                    85.7%;
                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                            7
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Matches 6; Conserv
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Pred. No. 3.4e+02;

85.78;

1; Mismatches

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Best Local Similarity 85.77
Matches 6; Conservative
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42 IOPPPLP 48
                                            1 MOPPPLP
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Matches
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                                                                                                                                                                                                     Leishmania major.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen G.J., Sogin M.L.,
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2203) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                             STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 2; Length 1404;
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 69 26179 26778.
Glardia lamblia ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                                   "A physical map of the Leishmania major Friedlin genome.", Genome Res. 8:135-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
NON TER 1 1
SEQUENCE 1404 AA; 152867 MW; 25F42AB6702B9D3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G., Submitted (CGT-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL445943; CAC14319-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 AA; 22317 MW; 1C303F8C087DAA4B CRC64;
                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein L5882.01 (Fragment).
                                                                                                     PRT; 1404 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
EMBL, AACB01000128; EAA37757.1; -.
InterPro, IPR008493; DUF775.
InterPro, IPR011024; G_crystallin_SF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 85.7
nes 6; Conservative
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                                                                                                     PRELIMINARY;
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1142 LQPPPLP 1148
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184 LQPPPLP 190
   1 MOPPPLP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MOPPPLP 7
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                     Q9GRR6
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                                                                       RESULT 13
C9GRRG.
AC 09GRR
AC 09GRR
DT 01-MA
RP SEQUE
RR SERAI
RA DM
RL Genor
RN Smith
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RN SMITH
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RY RA MASSU,
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RY RAJET
RY SUDMI
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90.5%; Score 38; DB 2; Length 199;

Query Match

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                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P0412D08.6 (Hypothetical protein
P0035F08.28).
Name=P0412D08.6; Synonyms=P0035F08.28;
Oryza satiav (japonica cultivar-group).
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.5%; Score 38; DB 2; Length 256
85.7%; Pred. No. 4.4e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005499; BAD03682.1; -.
EMBL; AP004746; BAD03407.1; -.
Hypothetical protein.
SEQUENCE 256 AA; 27545 MW; C9FB63C981F7B0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Katayose Y., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 12, 2005, 08:05:35 Job time : 36.2182 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 85.7 nes 6; Conservative
PRELIMINARY;
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166 VQPPPLP 172
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Sasaki T., Matsumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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us-10-691-330-2.rag

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model • OM protein

April 12, 2005, 07:49:31 ; Search time 95.2 Seconds (without alignments) 69.064 Million cell updates/sec Run on:

US-10-691-330-2 89 Title: Perfect score: Sequence:

1 LQTPQPLLQVMMEPQGD 17 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Gapop 10.0 , Gapext 0.5 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04;* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOMMAKIES	Description	l Aab72501 Colostrin) Aab59310 Ewe colos	7 Aab72247 Colostrin	3 Aab72533 Colostrin	Aa014578	7 Aam51037 Colostrin	9 Aae20229 Colostrin	Adn60296	5 Ads74386 Ovine col	1 Aab59341 Ewe colos	5 Aae07185 Colostrin	5 Aae07195 Modified			Abp30759	Abu46454	Abu44329 Protein e	Abb55615	3 Adr96210 Novel S.	Aaw80722 S. pneumo	Aau37640 Str	3 Aam01093 CFE 96 pr	Abu00620 S.	O Abu45840 Protein e	Adg73361 Streptoco
SOME	ID	AAB72501	AAB59310	AAB72247	AAB72533	AA014578	AAM5103	AAE20229	ADN60296	ADS74386	AAB5934	AAE07185	AAE07195	AB064584	ABP27487	ABP30759	ABU46454	ABU44329	ABB55615	ADR96210	AAW80722	AAU37640	AAM01093	ABU00620	ABU45840	ADG73361
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*	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	62.9	65.9	57.3	53.9	53.9	53.9	53.9	53.9	51.7	51.7	51.7	51.7	51.7	51.7	51.7
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Gaps

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Length 17; Indels

Query Match
100.0%; Score 89; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0;

Sequence 17 AA;

693 7 ADC73484 693 8 ADK47562 83 4 AAM15539 83 4 AAM3029 83 4 AAB29372 83 4 AAB19955 83 4 AAM57329 83 4 AAM55322 83 4 AAM5532 83 4 AAM5532 83 4 AAM45532 83 4 AAM45532 83 6 AAM48760 667 2 AAW48760 133 2 AAY07279 134 8 ADP86572	Adg73484 Streptoco	Adk47562 Streptoco	Aam15539 Peptide #	Abb34546 Peptide #	Aam28029 Peptide #	Abb29372 Peptide #	Abb19955 Protein #	Aam67729 Human bon	Aam55332 Human bra	Abg49367 Human liv	Aam03288 Peptide #	Abg37289 Human pep	Adi26093 Human pro	Adi26091 Human pro	Aaw48760 BOP1 prot	Adi26095 Human pro	Aao29916 Human bet	Aay07279 Bovine sy	Aay07278 Human bet	Adp86572 Human bet
	ADG73484	ADK47562	AAM15539	ABB34546	AAM28029	ABB29372	ABB19955	AAM67729	AAM55332	ABG49367	AAM03288	ABG37289	ADI26093	ADI26091	AAW48760	AD126095	AA029916	AAY07279	AAY07278	ADP86572
	93 7	93 8	33 4	33 4	33 4	33 4	33 4	33 4	33 4	33 4	33 4	33 5	_	_	•	_	_	33 2	34 2	34 8
	51.7	51.7	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.6	49.4	49.4	49.4	49.4
$\begin{array}{c} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 &$	46	46	45	45	45	45	45	45	45	45	45	45	45	45	45	45	44	44	44	44
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidating species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient
                                                                                                                                                                                                                                                                                                                                                                                              Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations.
                                                                                                                      Dermatological; oxidative stress regulator; colostrinin.
                                                                                                                                                                                                                                                                                                                                       Boldogh I;
AAB72501 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 25; 48pp; English.
                                                                                                                                                                                                                                              17-AUG-2000; 2000WO-US022665.
                                                                                                                                                                                                                                                                            99US-0149310P
                                                           (first entry)
                                                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                      Stanton GJ, Hughes TK,
                                                                                       Colostrinin peptide #2.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-218342/22.
                                                                                                                                                                                 WO200112650-A2.
                                                                                                                                                   Unidentified.
                                                                                                                                                                                                                                                                            17-AUG-1999;
                                                           09-MAY-2001
                                                                                                                                                                                                               22-FEB-2001.
                            AAB72501;
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AAB59310;

RESULT 2

AAB5931

Ovis sp.

Sheep;

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Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin, a proline rich polypeptide aggregate contained in colostrum. The peptides have immune response medulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing cytokines production, for medulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders of the central nervous system, neurological Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic acquired immunological deficiencies
     neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                                                                                                                                                                                                                                                                                                  Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuroprotective; neural cell differentiation regulator; colostrinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 89; DB 4; Length 17; 100.0%; Pred. No. 3.2e-07;
                                                                                                                                                                                                                                                                                                            Georgiades J;
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                                                                                                                                                                                                                                                                                                            Boldogh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB72533 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                                                                 (TEXA ) UNIV TEXAS SYSTEM.
(REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LOTPOPLLOVMMEPOGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                            17-AUG-2000; 2000WO-US022818
                                                                                                                                                                                                               99US-0149311P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-2000; 2000WO-US022774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
Local 7; Conservative
                                                                                                                                                                                                                                                                                                           Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colostrinin peptide #2.
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-202804/20.
                         infection
                                                                                                 WO200111937-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200112651-A2
                                                                                                                                                                                                               17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2001.
                                                                                                                                      22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               regulator.
     dementia;
                         neurosis;
                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colostrum
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                                                                                                                                                                                                                                                                                 Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colostrinin derived cytokine inducing peptide SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 89; DB 4; I Local Similarity 100.0%; Pred. No. 3.2e-07; Ne 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               Ewe colostrinin peptide fragment A-1.
                                                                                                                              AABS9310 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB72247 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGE-) REGEN THERAPEUTICS PLC.
17
                                 LOTPOPLLOVMMEPOGD 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-00012852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2000; 2000WO-GB002128
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                                                                                                                                                                                                                                                                                                                                                                              WO200075173-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-1999;
                                                                                                                                                                                                       21-MAR-2001
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AAB72247;

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RESULT 3 AAB72247

Query Match

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Gaps

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Indels

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                                                                                                                                      (first entry)
                                                                           Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-269150/31.
                                                        Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        WO200213849-A1
                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                      30-MAY-2002
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                                                                                                                                                                                                                                 AAM51037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a method for promoting cell differentiation (e.g. neural cell differentiation). The method involves contacting cells with a neural cell regulator (i.e. a colostrinin peptide) in order to change the cells in morphology to form neural cells. Colostrinin is a proline-rich polypeptide aggregate that is present in colostrum. The method of the
                                                                  Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                    The present invention relates to a method for promoting neural cell adifferentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                        cell differentiation; neural cell regulator; colostrinin peptide; cell formation; proline-rich polypeptide aggregate; colostrum; cell treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Promoting cell differentiation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                    100.0%; Score 89; DB 4; Length 17; 100.0%; Pred. No. 3.2e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                  AAO14578 standard; peptide; 17 AA
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                                                                                                                Claim 6; Page 21; 35pp; English.
                                                                                                                                                                                                                                                                                     LQTPQPLLQVMMEPQGD 17
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(TEXA ) UNIV TEXAS SYSTEM
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nes 17; Conservative
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                                           WPI; 2001-226545/23
                                                                                                                                                                                               Sequence 17 AA;
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Modified-site
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                     Boldogh I;
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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. Methods are claimed for: regulator in claimed methods of the invention. Methods are claimed for: inducting a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell by contact with the immunological regulator. Conganism, and the cell is mammalian, including human; modulating an immune conditions effective to induce a cytokine; modulating an immune conditions effective to induce a cytokine, where the immunological regulator under conditions effective to induce a cytokine, where the immunological conditions effective to induce a cytokine, where the immune response is specific or non specific, an interferon cand where the immune response is specific or non specific, an interferon contacting blood cells with a blood cell regulator, where the blood cells when a cell culture or an organism, are mammalian or human, and where the blood cells are increased in number or differentiated; and a method for modulating blood cell proliferation in a patent. A claimed
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invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                   5; Length 17;
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blood cell regulator; cytokine inducer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optional C-terminal amidation"
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100.0%; Pred. No. 3.2e-07;
ive 0; Mismatches 0;
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(REGE-) REGEN THERAPEUTICS PLC.
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organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide

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Gaps

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Length 17; Indels

Score 89; DB 5; I Pred. No. 3.2e-07;

Mismatches

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100.0%; ilarity 100.0%; Conservative 0

Query Match Best Local Similarity Matches 17; Conserv

Sequence 17 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
cytokine-inducing composition comprises a pharmaceutical carrier and active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 an interleukin-12. It was one of the best overall inducers in almost all cytokine and blood cell proliferation experiments conducted
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100.0%; Pred. No. 3.2e-07;
tive 0; Mismatches 0;
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Matches 17; Conserv
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Modified-site
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Constituent peptide of colostrinin SEQ ID NO:2.

(first entry)

29-JUL-2004

ADN60296 standard; peptide; 17 AA.

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The present invention describes the use of a modulator selected from colostrinin, its constituent peptide, its active analogue, and a combination of these, for modulating an intracellular signaling molecule in a cell, down regulating 4HRE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, protecting against DNA damage in a cell, inhibiting apoptosis in a cell, protecting against DNA damage in a cell. The modulator has cytostatic activity, and can be used as a 44NR inhibitor. The modulator is useful in the manufacture of a medicament for reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated plutathione depletion, inhibiting 4HNE-mediated activation of c-Jun NH2-terminal kinases. Colostrinin, or its constituent peptide or active analogue is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of colostrinin for e.g. modulating an intracellular signaling molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in a cell.
                                                                                                                              modulator; colostrinin; intracellular signaling molecule modulator; 4HNB-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNB inhibitor; 4HNB-protein adduct formation reduction; 4HNB-mediated glucathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
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) STANTON J G.
) GEORGIADES J A.
' TITCHES T K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanton JG,
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(HUGH/)
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inhibiting apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The present sequence represents a synthetic constituent peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and
                                The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
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                                                                                                      8; Length 17;
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                                                                                                     100.0%; Score 89; DB 8; I
100.0%; Pred. No. 3.2e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                   ADS74386 standard; peptide; 17 AA.
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08-MAR-2004; 2004GB-00005190.
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                                                                                             Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                            Ovine colostrinin peptide
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                                                                           Sequence 17 AA;
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ADS74386
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheep, colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
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                                    Score 89; DB Pred. No. 3.26; Mismatches
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                                    100.0%;
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                              Query Match
Best Local Similarity
Matches 17; Conserv
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Sequence 17 AA;
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Local Sim-
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ID AAE0
XX
AC AAE0
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us-10-691-330-2.rag

Colostrinin, nootropic, neuroprotective; immunomodulatory; antibacterial; Parkinson's disease; Alzheimer's disease; mental disorder; food additive; central nervous system disorder; neurodegenerative disorder; weight loss; beta-amyloid plaque; psychosis; neurosis; cachaxia; motor neuron disease; acquired immunological deficiency; neurological disorder; dementia;

Modified colostrinin cyclic peptide #1.

/note= "N-terminal acetyl; this residue forms a cyclic linkage with Gln found at the C-terminal end"

WO200155199-A1

02-AUG-2001

Location/Qualifiers

Key Modified-site

antiviral; cyclic

Synthetic.

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The invention relates to colostrinin peptide fragments which are useful, in the treatment of chronic disorders of the immune system. Cand the central nervous system. Colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., Alzheimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g., parkinson's disease, mental disorders e.g. psychosis and neurosis, in acquired immunological deficiencies, chronic bacterial and ral infections and diseases characterised by the presence of betal amylosing plaques and as a distary supplement for babies, small children, amylosing paginges and as distary supplement for babies, small children, have suffered from cacheary supplement for babies, small children, have suffered from cacheary or have subjected to chemotherapy or have suffered from cacheary or used as food additives and as an auxillary withdrawal treatment for drug addicts, after a period of detoxification and in persons dependent on stimulants. Colostrinin peptides are used to prepare antibodies and to treat emotional disturbances, e.g. emotional disturbances of psychiatric patients in a state of depression. These colostrinin peptides improves the immunological deficiencies in a child. The
                                                                                                         Colostrinin, nootropic; neuroprotective; immunomodulatory; antibacterial; Parkinson's disease; Alzheimer's disease; mental disorder; food additive; central nervous system disorder; neurodesgenerative disorder; weight loss; beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease; acquired immunological deficiency; neurological disorder; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s improves the development of immune system in a new prrect the immunological deficiencies in a child. The colostrinin peptide 1 related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.9%; Score 56; DB 4; Length 11; 100.0%; Pred. No. 0.039; 1ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2000; 2000GB-00001825.
                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-2001; 2001WO-GB000329.
                   (first entry)
                                                              Colostrinin peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488775/53.
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
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                                                                                                                                                                                                                                                                       Unidentified
                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                          antiviral.
%XCCCCCCCCCCCCCCCCCCCCX
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(REGE-) REGEN THERAPEUTICS PLC. 26-JAN-2000; 2000GB-00001825. 26-JAN-2001; 2001WO-GB000329.

WPI; 2001-488775/53.

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The invention relates to colostrinin peptide fragments which are useful, inter alia, in the treatment of chronic disorders of the immune system and the central nervous system. Colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., larbeimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g., packosis and neurosis, in acquired immunological deficiencies, chronic bacterial and curvosis, in acquired inwholave been subjected to chemotherapy or amyloid plaques and as a dietary supplement for babies, small children, adults and senile persons, who have been subjected to chemotherapy or chave suffered from cachexia or weight loss due to the chronic disease. Colostrinin peptides are also used as food additives and as an auxillary withdrawal treatment for drug addicts, after a period of detoxification and in persons dependent on stimulants. Colostrinin peptides are used to prepare antibodies and to treat emotional disturbances, e.g. emotional colostrinin peptides improves the development of immune system in a new colostrinin peptide improves the development of immune system in a new person the immunological deficiencies in a child. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.9%; Scc.
100.0%; Pre
0; }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 8; 40pp; English
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Best Local Similarity
Matches 11; Conserv
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ABO64584
ID ABO64
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AC ABO64
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Gaps . 0

Conservative OPLLQVMMEPQ 15

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OPLLOVMMEPO

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AAE07195 standard; peptide; 12

RESULT 12 AAE07195 (first entry)

06-NOV-2001

AAE07195;

BXXXEX

Fraser C;

us-10-691-330-2.rag

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5481 sequences (51), given in the specification. The proteins have antibacterial and antimilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus in a nucleic acid encoding (I) are used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I) may be used to defermine whether a compound by Streptococcus that is prevented or treated may be monightis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.9%; Score 48; DB 5; Length 692; 40.0%; Pred. No. 60; tive 8; Mismatches 1; Indels
                                                                                                    Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus polypeptide SEQ ID NO 10694.
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3571; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP30759 standard; protein; 692 AA.
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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07-MAR-2001; 2001GB-00005640.
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400 IEVPEPVIQLMVEPK 414
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                                        (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC
                                                                                                                                                                WPI; 2002-352536/38.
N-PSDB; ABN68118.
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tes 6; Conserv
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                                                                                                                             rettelin H;
                                                                                                      relford J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial, antinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                      Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
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Pred. No. 2.1;
?; Mismatches 2; Indels
                                                              Klebsiella pneumoniae polypeptide segid 11101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 11101; 932pp; English
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                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP.
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2000GB-00028727.
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                    (first entry)
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Best Local Similarity 69.2.
Pest Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Breton GL, Osborne M;
                                                                                                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-895346/82.
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24-NOV-2000;
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                    29-JUL-2004
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Gaps

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(GENO-) INST GENOMIC RES
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Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C; Tettelin H;

WPI; 2002-352536/38

N-PSDB; ABN71390

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.

Claim 1; Page 4179; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71236 and antibacise that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins

Sequence 692 AA;

0; Gaps 53.9%; Score 48; DB 5; Length 692; 40.0%; Pred. No. 60; iive 8; Mismatches 1; Indels 1; Indels Query Match
Best Local Similarity 40.0
Matches 6; Conservative

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1 LOTPOPLLOVMMEPQ 15

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Facence 11101, Application US/09489039A

Facence 11101, Application US/09489039A

Facence 11101, Application US/09489039A

GENERAL INFORMATION:

APPLICANT GATY BECON Et. al

ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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US-09-489-039A-11101
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Sequence 26848, A
Sequence 26848, A
Sequence 4077, Ap
Sequence 2, Appli
Sequence 25420, A
Sequence 35942, A
Sequence 3159, A
Sequence 2224, A
Sequence 22224, A
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                                                                                                                                                                                                                                                            April 12, 2005, 07:49:30 ; Search time 19:9364 Seconds (without alignments) 63.654 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-270-767-2542
US-09-270-767-35942
US-09-270-767-35942
US-09-270-767-3159
US-09-248-795A-18983
US-09-248-795A-18983
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US-09-248-795A-18983
US-09-248-795A-18983
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Database

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Sequence 2, Application US/09641803

Facture No. 6500798

GENERAL INFORMATION:
FAPPLICANT: STANTON, G. John
APPLICANT: BOLDOGH, ISTVAN
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT FILING DATE: 2000-08-17
FRIOR RIPLING DATE: 1999-08-17
FRIOR FILING DATE: 1999-08-17
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 17
FRIOR LINE APPLICATION VANDER: 60/149,310
FRIOR FILING DATE: 1999-08-17
SEQ ID NO 2
LENGTH: 17
FRIOR LINE APPLICATION VANDER: 60/149,310
FRIOR FILING DATE: 1999-08-17
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                                                           Sequence 23561, A Sequence 42966, A Sequence 15. Apple 200 Sequence 30333 A Sequence 4213, Apple 200 Sequence 4213, Apple 200 Sequence 31345, Apple 200 Sequence 31345, Apple 200 Sequence 41815, Apple 200 Sequence 41815, Apple 200 Sequence 41815, Apple 200 Sequence 41815, Apple 200 Sequence 41848, Apple 200 Sequence 41848, Apple 200 Sequence 6366, Apple 200 Sequence 636
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100.0%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                         US-09-855-323-15
US-09-525-991A-30333
US-09-513-9996-6328
US-08-813-207A-456
US-09-107-4213
US-09-107-431345
US-09-255-991A-31345
US-09-285-1738-38
US-09-285-1738-38
US-09-286-1738-38
US-09-286-1738-38
US-09-270-767-41835
US-09-270-767-41835
US-09-270-767-41835
US-09-489-033A-41835
US-09-489-033A-10892
US-09-543-681A-6366
-09-328-352-7812
-09-252-991A-23561
-09-270-767-42966
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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-05-12
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; Patent No. 5876972
; GENERAL INFORMATION:
APPLICANT:
; TITLE OF INVENTION: Nucleic acid molecules coding for mammalian
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Pred. No. 35;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...471
SEQUENCE DESCRIPTION: SEQ ID NO: 4845:
                                            FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCS/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 40.0%; Pred. No. 6; Conservative 7; Mismatcl
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                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 4845:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 471 amino acids
TYPE: amino acid
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178 INVPEPVIQLMVEPK 192
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-08-718-661-2
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Sequence (2014)
Sequence (2014
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Sequence 4845, Application US/09107433
Sequence 4845, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF THVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
SOFTHARR: «Unknown»
SOFTHARR: «Unknown»
SOFTHARR: «Unknown»
TULICATION NUMBER: US/09/107,433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
                                                                                                                                                                   Score 51; DB 4
Pred. No. 0.54;
                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.7%; Score 46; DB Best Local Similarity 41.2%; Pred. No. 2.6; Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100 Beaver Street
LENGTH: 82
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LQTPQPLLQVMMEPQGD 17
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5206
                                                                                                                                                               Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                    1 LOTPOPLLOVMME 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
                                                                                               US-09-489-039A-11101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-248-796A-26848
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Sequence 18983, Application US/09248796A

Sequence 18983, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT RAPLICATION NUMBER: US/09/248,796A

CURRENT RILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18983

LENGTH: 230
                                                                                                                                                                                                                                                                        Sequence 51159, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51159
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 141;
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                                                                          DB
                                                                                          Pred. No. 26;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.2%; Score 42; DB Best Local Similarity 53.3%; Pred. No. 44; Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                    Query Match
Best Local Similarity 52.9%; Pred. No.
Matches 9; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42;
Pred. No.
              ), ORGANISM: Drosophila melanogaster
US-09-270-767-35942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Drosophila melanogaster US-09-270-767-51159
                                                                                                                                                 1 LOTPOPLLOVMMEPQGD 17
                                                                                                                                                                                       7 LOTTDMLVQVALQPQID 23
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ilarity 52.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Candida albicans
US-09-248-796A-18983
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Best Local Similarity
9; Conserva
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US-09-248-796A-22224
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US-09-270-767-51159
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GREERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25420
tumor suppressor proteins and methods for their isolation
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                                                                                                                                                                                                                                                                                                                                                                 50.6%; Score 45; DB 2; Length 667; 60.0%; Pred. No. 48;
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                   CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 LPVPÓPLPÓPOMOPÓ 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LQTPQPLLQVMMEPQ 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 60.v.
Post Source 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                LENGTH: 667 amino acids
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PQPLLQPLLQP 19
              NUMBER OF SEQUENCES: 1:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-718-661-2
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INVENTION:
                                                                                                                                                                                                                                                                      amino acid
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US-09-248-796A-25420
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APPLICANT: Stassi, Diane L.
APPLICANT: Stamsi, Diane L.
APPLICANT: Stamsi, Diane L.
APPLICANT: Ruan, Xiaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Rekavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES:
ADDRESSE: Abbott Labrari
                                                                                                                                     12;
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                                                                                       Score 41; DB 4; Length 294;
Pred. No. 83;
4; Mismatches 2; Indels
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46.1%; Score 41; DB 3; Length 343;
Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                        1 LQTPQ-----PLL-----QVMMEPQGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/858,003
FILING DATE: 16-MAY-1979
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4952.US.P2
                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08858003 Patent No. 6060234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Abbott Laboratories
100 Abbott Park Rd.
                       ; ORGANISM: Acinetobacter baumannii
US-09-328-352-7430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: No. 6060234e
                                                                                  Query Match 46.1%;
Best Local Similarity 37.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QTPQPLLQVMMEPQG 16
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42 QLPRPLKDVLFAPEG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                      US-08-858-003-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-858-003-32
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US-09-078-166-32
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Sequence 22224, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
FILLE OF INVENTION:
FILLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
FILLE REPERENCE: 10799-02-12
CURRENT FILING DATE: 1999-02-13
FRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PELLONG DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22224
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7430, Application US/09328352
Batent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7430
LENGTH: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%; Score 41; DB 4;
47.1%; Pred. No. 25;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: No. 64037834, Julia E.
TITLE OF INVENTION: Tumor Marker Zsig62
FILE REPERENCE: 98-76
CURRENT APPLICATION NUMBER: US/09/493,565
CURRENT FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09493565
Patent No. 6403783
GENERAL INFORMATION:
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59 RPLLQGCEDIMVQPEGD 75
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160 IPSPEPLLEPLLEP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LQTPQPLLQVMMEP 14
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Candida albicans
US-09-248-796A-22224
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.9
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 8; Conserv
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Sequence 32, Application US/09079166

GRANEAL INFORMATION:
APPLICANT Stass, Disage L.
APPLICANT NUMBERS:
APPLICANT NUMBERS:
APPLICANT NUMBERS:
APPLICANT NUMBERS:
APPLICANTON NUMBER:
APPLICATION NUMBER:
A
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Query Match 46.1%; Score 41; DB 3; Length 343;
Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps
Qy 2 QTPQPLLQVWMEPQG 16

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2 QTPQPLLQVNMEPQG 16 | |: || |: |: | 42 QLPRPLKDVLPAPEG 56

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Search completed: April 12, 2005, 08:07:49 Job time : 20.9364 secs

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1

equence 10, Appl Sequence 824, App Sequence 126258,

Sequence 10, Appl Sequence 64, Appl Sequence 94, Appl Sequence 94, Appl Sequence 90, Appl Sequence 10, Appl Sequence 2, Appl Sequence 900, Appl Sequence 900, Appl Sequence 91, Appl Sequence 92, Appl Sequence 57461, Appl Sequence 61020, Appl Sequence 57461, Appl Sequence 57461, Appl Sequence 57461, Appl Sequence 57461, Appl Sequence 5760, App

Sequence 3898, Ap Sequence 46468, A

Perfect score: Sequence: Scoring table:

Run on:

Searched:

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GENERAL INFORMATION: US20030091606A1

| Sequence 2. Application US/10281652
| Publication No. US20030091606A1
| GENERAL INFORMATION: G. John
| APPLICANT: STATYON, G. John
| APPLICANT: BOLDOGH, IStvan
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
| TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
| FILE REPERENCE: 265.00220101
| TURENT APPLICATION NUMBER: US/10/281,652
| CURRENT FILING DATE: 2000-08-17
| PRIOR FILING DATE: 2000-08-17
| PRIOR FILING DATE: 1999-08-17
| NUMBER OF SEQ ID NOS: 34
| SEG ID NO 2
| LENGTH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 89; DB 14; Length 17; 100.0%; Pred. No. 4.5e-07; Live 0; Mismatches 0; Indels
              5 US-10-374-780A-824
6 US-10-374-780A-824
6 US-10-437-963-126258
0 US-10-629-963-106
0 US-09-782-974C-68
7 US-10-467-492A-68
7 US-10-9782-974C-94
7 US-10-921-590-90
7 US-10-921-590-90
7 US-10-921-590-90
7 US-10-921-590-90
8 US-10-272-983-10
9 US-10-373-807-10
9 US-10-373-807-10
9 US-10-373-807-10
9 US-10-373-807-10
9 US-10-373-807-10
9 US-10-373-807-10
9 US-10-10-398-900
9 US-10-298-900
9 US-10-288-122A-5162
9 US-10-288-122A-5162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
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US-10-281-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 17
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Sequence 1, Appli
Sequence 1, Appli
Sequence 74378, A
Sequence 72253, A
Sequence 13233, A
Sequence 3744, App
Sequence 374, App
Sequence 3253, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                    April 12, 2005, 07:49:30 ; Search time 52.7 Seconds (without alignments) 107.096 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1. \( \text{cgn2} \) \( \frac{6}{\text{pt} \text{cdata}} \) \( 1/\text{pubpaa} \) \( 1/\text{pubpaa} \) \( 1/\text{cgn2} \) \( \frac{6}{\text{pt} \text{cdata}} \) \( 1/\text{pubpaa} \) \( 1/\
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1418010
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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7 US-10-691-330-2

6 US-10-182-110-1

5 US-10-282-122A-74378

5 US-10-282-122A-73253

• US-09-815-242-13233

• US-09-815-242-13233

• US-10-282-122A-73764

7 US-10-472-928-374

6 US-10-767-701-49828

• US-09-864-761-35253

• US-09-864-761-35253

• US-09-824-761-35253

• US-10-826-157-4

• US-10-826-157-4

• US-10-425-114-51657
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                                                                                                                                                                                                                                                                                                                                                                                                           1418010 segs, 331997259 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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89
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Match Length DB
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533.9
51.77.7
51.77.7
50.6
50.6
64.9
64.9
64.9
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Gaps

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Result

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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/200,848
FRIOR FILING DATE: 2000-03-21
FRIOR PELING DATE: 2000-05-28
FRIOR PELING DATE: 2000-05-28
FRIOR PELING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR PLING DATE: 2000-09-06
FRIOR PELING DATE: 2000-09-09
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: 60/257, 636
FRIOR PELING DATE: 2001-02-09
FRIOR PELING DATE: 2001-02-09
FRIOR PELING DATE: 2001-02-16
FRIOR PELING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR PELING DATE: 2001-02-16
FRIOR FILING DATE: 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 59;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72253, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Volsen, Kari
APPLICANT: Volsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, paniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48;
Pred. No. !
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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illarity 40.0%;
Conservative
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                                                                                                                                                                                                                                                                     Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                             Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                 CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
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                                                                                                                                                                  APPLICANT: Stancon, G. John
APPLICANT: Stancon, G. John
APPLICANT: Bughes, Thomas K., Jr.
APPLICANT: Hughes, Thereor As Inhibitors of Apoptosis and Other Cellulal
TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAN
FILE REFERENCE: 265.00390101
CURRENT APPLICATION NUMBER: US/10/691,330
CURRENT FILING DATE: 2003-10-22
PRIOR PAPLICATION NUMBER: US 60/420,369
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.9%; Score 56; DB 16; Length 11; Best Local Similarity 100.0%; Pred. No. 0.039; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-2
                                              Sequence 2, Application US/10691330
Publication No. US20050042300A1
GENERAL INFORMATION:
APPLICANT: Boldogh, Istvan
APPLICANT: Stanton, G. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LQTPQPLLQVMMEPQGD 17
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial
                            US-10-691-330-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 17
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

US-10-282-122A-74378 ; Sequence 74378, Application US/10282122A ; Publication No. US20040029129A1

RESULT 4

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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITARA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR PLILNG DATE: 2000-03-21

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR PLILNG DATE: 2000-09-06

PRIOR PLILNG DATE: 2000-09-06

PRIOR PLILNG DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/250,636

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-10-29

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR 
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                                                                                                                                                                                                                                                                                                             Length 693;
                                                                                                                                                                                                                                                                                                                                                 1.2e+02;
                                                                                                                                                                                                                                                                                                             51.7%; Score 46; DB 9; 40.0%; Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13233
; LENGTH: 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 73764, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae US-,10-,282,122A-73764
                                                                                                                                                          TYPE: PRT; CRGANISM: Streptococcus pneumoniae
US-09-815-242-13233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
Xu, H.
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Best Local Similarity 40.0%
Conservative
Conservative
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                                                                     PRIOR PELLING DATE: 2003-02-20
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-01-23
PRIOR PELLING DATE: 2000-01-23
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-16
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APPLICANT: CATT, CTANT C.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PRACTYCLES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.9%; Score 48; DB 40.0%; Pred. No. 60; tive 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptococcus mutans
US-10-282-122A-72253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: |:|:|:||:
400 IEVPEPVIQLMVEPK 414
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LQTPQPLLQVMMEPQ 15
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Best Local Similarity
Matches 6; Conserva
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400 INVPEPVIQLMVEPK 414

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APPLICANT: Xovalio, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cab, Yongwa
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 18-21/33535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 49828
LENGTH: 74
             Sequence 374, Application US/10472928

Publication No. US20050020813A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH

TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: P026926M0

CURRENT FILING DATE: 2003-09-26

CURRENT FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: US/10/472,928

PRIOR APPLICATION NUMBER: GB-0107658.7

NUMBER OF SEQ ID NOS: 4979

SOFTWARE: SeqWin99, version 1.03

LENGTH: 693
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OTHER INFORMATION: translation elongation factor G (fusA)
OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15902294 (0.E+01)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3478-017-P1-K1-G5.pep
US-10-767-701-49828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49828, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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US-09-864-761-35253
; Sequence 35253, Application US/09864761
; Patent No. US20020048763A1
; GENBEAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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400 INVPEPVIQLMVEPK 414
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Matches 6; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0-767-701-49828
10-472-928-374
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Sequence 10, Application US/09789054A

Sequence 10, Application US/09789054A

Sequence 10, Application US/09789054A

Sequence 10, Application No. US20020184659A1

GENERAL INFORMATION:

APPLICANT: Allen, Steve

TITLE OF INVENTION: FRANSCRIPTION

TITLE OF INVENTION: FRANSCRIPTION

TITLE OF INVENTION: FRANSCRIPTION

FILE REFERENCE: BB1107 US CIP

CURRENT FILING DATE: 2001-02-20

PRIOR PLING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: CT/US98/16688

PRIOR PLING DATE: 1999-08-15

PRIOR APPLICATION NUMBER: CCT/US98/16688

PRIOR PLING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Microsoft Office 97

LENGTH: 296
APPLICANT: Zhou, Yingdong
APPLICANT: Kovalid, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 549
TYPE: N.
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Pred. No. 1.4e+02;
1; Mismatches 4
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49.4%; Score 44; DB 15;
Best Local Similarity 56.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 2; Mismatches 5
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Publication No. US20040019927A1
GENERAL INFORMATION:
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APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
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Best Local Similarity 64.3%;
Matches 9; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
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US-10-374-780A-824
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                                                                                                                                                                                             Sequence 2, Application US/10223978
Publication No. US20030125522A1
GENERAL INFORMATION:
APPLICANT: Atgen Co., Ltd.
APPLICANT: Rim, Jong-Sun
TITLE OF INVENTION: Proteins Including Said Peptides
TITLE OF INVENTION: Proteins Including Said Peptides
TITLE OF INVENTION: Proteins Including Said Peptides
CURRENT APPLICATION UNDBER: US/10/223,978
CURRENT PILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: PEPTIDE
; LOCATION: (1)...(50)
; OTHER INFORMATION: Acidic tail amino acid sequence 85-134 of beta-synuclein
US-10-223-978-2
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APPLICANT: Lindquist, Susan L.
APPLICANT: Outeiro, Tiago
JITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
FILE REFERENCE: 17481-003001
CURRENT APPLICATION NUMBER: US/10/826,157
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/472,317
PRIOR APPLICATION NUMBER: US 60/463,284
PRIOR APPLICATION NUMBER: US 60/463,284
PRIOR FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 134
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Pred. No. 43;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.4%; Score 44; DB 14; Length 50; Best Local Similarity 46.2%; Pred. No. 15; Matches 6; Conservative 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10826157; Publication No. US20050064548A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%;
                                                                                                          21 LOKPOPLLASLASPO 35
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105 EPLIEPLMEPEGE 117
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21 EPLIEPLMEPEGE 33
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; ORGANISM: Homo sapiens
US-10-826-157-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserva
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US-10-425-114-51657
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US-10-223-978-2
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Gaps
Heard, Jacquet.
Haake, Volbert A

Crealman, Robert A

T. Ratcliffe Joliver

T. Adam Luc J James

ATT: Reuber, T Lynne

ATT: Reuber, T Lynne

ATT: Reuber, T Lynne

ATT: Pilogin, Marsha L

CANTT: Pilogin, Marsha L

CANTT: Dincal, Omalta

LE OP THVENTION: POLYNUCEDCIDES AND POLYPEPTIDES IN PLANTS

LE REPRERNCE: MARSH 1047 CIP

ARENT PAPLICATION NUMBER: 09/337,944

PRIOR FILING DATE: 2000.04-09

PRIOR FILING DATE: 2000.04-09

PRIOR PLICATION NUMBER: 09/336,49

PRIOR PLICATION NUMBER: 06/336,049

PRIOR PLICATION NUMBER: 06/336,049

PRIOR PLICATION NUMBER: 06/336,049

PRIOR PLICATION NUMBER: 00/225,066

PRIOR PLICATION NUMBER: 10/225,066

PRIOR PLICATION NUMBER: 10/225,066

PRIOR PLILING DATE: 2002-06-14

PRIOR PLILING DATE: 2002-06-19

PRIOR PLILING DATE: 2002-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QTPQPLLQVMMEPQ 15
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Search completed: April 12, 2005, 07:55:20 Job time : 52.7 secs

199 ОТРОРОРОЙНРОРО 212

g

Tue Apr 12 09:04:55 2005

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

April 12, 2005, 07:49:31 ; Search time 12.2091 Seconds (without alignments) 133.973 Million cell updates/sec Run on:

US-10-691-330-2 89 1 LQTPQPLLQVMMEPQGD 17 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		عن				
Regult No.	Score	Query Match	Length	08	Ω	Description
-	48	53.9	709	7	D86907	nga
7	47.5	53.4	192	7	AF1753	Orf50 [bacteriopha
М	46	⊣	639	~	S03268	tetracycline resis
4	46	51.7	693	N	B97903	elongation factor
2	46	51.7	693	7	B95032	translation elonga
9	44	49.4	134	~	844430	synuclein - human
7	44	49.4	134	~	S39046	phosphoneuroprotei
80	44	49.4	137	~	IS6498	phosphoneuroprotei
6	44	49.4	671	~	C96534	probable Poly-A Bi
10	43	48.3	134	~	AB0784	conserved hypothet
11	43	48.3	639	~	A60633	tetracycline resis
12	43	48.3	639	0	A56779	tetracycline resis
13	43	48.3	639	~	S13142	tetracycline resis
14	43	48.3	695	~	AE1406 .	
15	43	48.3	695	~	AE1782	
16	43	48.3	669	N	E97594	
. 17	43	48.3	669	~	AC2816	translation elonga
18	43	48.3	844	~	F86231	hypothetical prote
19	42	47.2	263	~	S74353	carbonic anhydrase
20	42	47.2	580	~	S13328	hypothetical prote
21	42	47.2	595	7	F85438	nucleoporin-like p
22	42	47.2	643	2	S55610	
23	42	47.2	698	~	C82332	translation elonga
24	41	46.1	78	~	D91160	hypothetical prote
25	41	46.1	78	~	C86006	1 pro
26	41	46.1	78	~	E65136	_
27	41	46.1	639	7	A24333	tetracycline resis
28	41	46.1	641	~	Ō	tetracycline-minoc
59	41	46.1	857	7	JC4169	phosphoenolpyruvat

UL52 protein - hum	hypothetical prote	hypothetical prote	hypothetical prote	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	hypothetical prote	hypothetical prote	hypothetical prote	lactoylglutathione	hypothetical prote	protein F1N21.10 (hypothetical prote	esterase, probable	translation elonga
WMBE52	B91052	F85896	G65028	S53427	JC4263	A55574	G72676	T14439	T14440	T47277	T21149	E96696	T38405	H87344	EFTWG
ч	~	N	7	~	Н	-	7	~	~	~	N	~	N	N	Н
1058	1653	1653	1653	549	929	929	237	259	282	284	300	357	357	380	691
46.1	46.1	46.1	46.1	45.5	45.5	45.5	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9
41	41	41	41	40.5	40.5	40.5	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

elongation factor G [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C,Species: Lactococcus lactis subsp. lactis C,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C; Accession: D86907

Figolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlichender Res. 11, 731-753, 2001
A,Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis say, Reference number: A86625; MUID:21235186; PMID:11337471
A,Rocession: D86907
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-709 <SNA
A,Residues: 1-700 <SNA
A,Residues: 1-70

C, Genetics

A;Gene: fusA C;Superfamily: translation elongation factor G; translation elongation factor Tu homolog

ö Gaps ö Length 709; 1; Indels Query Match 53.9%; Score 48; DB 2; Best Local Similarity 40.0%; Pred. No. 5.8; Matches 6; Conservative 8; Mismatches

1 LOTPOPLLQVMMEPQ 15 ð

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RESULT 2

Oriso Dacteriophage bill285] homolog lin2571 [imported] - Listeria innocua (strain Clip) CrSpecies: Listeria innocua CrDate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (crSpecies: Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (crspession: AF175) Erangeui, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker stalascience 294, 484-882, 2001 Erangeui, L.; Runst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Arathors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; MuID:21837279; PMID:11679669

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-192 <GLA>

A;Cross-references: UNIPROT:0928G4; GB:AL592022; PIDN:CAC97798.1; PID:g16415093; GSPDB:GA;Experimental source: strain Clip11262

C,Genetics: A,Gene: lin2571

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A;Molecule type: DNA*
Skosidues 1.-693 «KUR»
A;Cross-references: UNIPROT:Q97SQ3; GB:AE005672; PIDN:AAK74451.1; PID:g14971744; GSPDB:GN
A;Experimental source: btrain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: SP0273
C;Superfamily: translation elongation factor G; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NyAlternate names: brain-specific protein, 14K
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1994 #sequence_revision 05-May-1995 #text_change 09-Jul-2004
C;Accession: S39046; JU0238
R;Nakajo, S.; Tsukada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.
Bur. J Biochem. 217, 1057-1063, 1993
A;Title: A new brain-specific 14-kDa protein is a phosphoprotein. Its complete amino acic
A;Reference number: S39046; MUID:94039126; PMID:8223629
                                                                                                                                                            C;Species: Streptococcus pneumoniae.
C;Species: Streptococcus pneumoniae.
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95032
R;Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I soin, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q16143; GB: S69965; NID: 9546911; PIDN: AAB30860.1; PID: 9546912
                                                                                                                                        translation elongation factor G [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Homo sapiens (man)
Cibate: 07-Oct.1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Cibate: 07-Oct.344 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Cifacession: 844431
Ridakes, R.; Spillantini, M.G.; Goedert, M.
FEBS Lett. 345, 27-32, 1994
A;Tile: Identification of two distinct synucleins from human brain.
A;Reference number: 844430; MUID:94252398; PMID:8194594
A;Accession: 844430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 693;
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400 INVPEPVIQLMVEPK 414
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105 EPLIEPLMEPEGE 117
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Best Local Similarity 46.2
Matches 6; Conservative
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-134 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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A;Molecule type: mRNA
A;Residues: 1-134 <JAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                        Cypecies: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Accession: S03268
R;Sanchez-Pescador, R; Brown, J.T.; Roberts, M.; Urdea, M.S.
Nucleic Acids Res. 16, 1216-1217, 1988
A;Title: The nucleotide sequence of the tetracycline resistance determinant tetM from Ure A;Reference number: S03268; MUID:88144009; PMID:3344217
A;Reference number: S03268
A;Molecule type: DNA
A;Residues: 1-639 csAN>
A;Cross-references: UNIPROT:P09757; GB:U08812; EMBL:X06901; NID:g475983; PIDN:AAA73978.1
C;Genetics
A;Genetic code: SGC3
A;Genetic code: SGC3
C;Superfamily: translation elongation factor G; translation elongation factor Tu homology csTU>
C;Genetics
C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop
F;10-13/Region: GTP-binding MKXD motif
F;128-131/Region: GTP-binding SAK/L motif
F;128-131/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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B97903
elongation factor G [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B97903
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.; W.; M.; W.; W.; W.; W.; E. C.; E. C.; E. C.; Matsushima, P.; McAhren, S.; M.; Sun, P.; N.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Althors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Althors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Althors: Wolle-Lindary
A;Accession: B97903
A;Accession: B97903
A;Accession: B97903
A;Accession: B97903
A;Accession: B97903
A;Colecule type: DNA
A;Residues: 1-693 <KUR>
A;Colecule type: DNA

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                DB 2; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46, DB 2; Length 639;
Pred. No. 11;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%; Score 46; DB 2; Length 693;
40.0%; Pred. No. 12;
tive 7; Mismatches 2; Indels
                                                                                        Indels
        Score 47.5; DE Pred. No. 1.6; 5; Mismatches
                                                1.6;
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31 TPKPLPGGVEISVEPQGD 48
                                                                                                                                                            3 TPOPL---LOVMMEPQGD 17
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Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 40.0
Matches 6; Conservative
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Indels

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conserved hypothetical protein STY2446 [imported] - Salmonella enterica subsp. enterica s
Cypscies: Salmonella enterica subsp. enterica servoar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                    Cjaccession: AB0784
R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Aththors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A60633
R;Nesin, M.; Svec, P.; Lupski, J.R.; Godson, G.N.; Kreiswirth, B.; Kornblum, J.; Projan, Antimicrob. Agents Chemother. 34, 2273-2276, 1990
A;Title: Cloning and nucleotide sequence of a chromosomally encoded tetracycline resista. A;Reference number: A60633; MUID:91158314; PMID:2073121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:053770; GB:M21136; NID:9153114; PIDN:AAA26678.1; PID:9153115
C;Superfamily: translation elongation factor G; translation elongation factor Tu homolog
C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop
F;H-131/Domain: translation elongation factor Tu homology <ETU>F;10-17/Region: nucleotide-binding motif A (P-loop)
F;10-17/Region: GTP-binding MXC motif
F;220-222/Region: GTP-binding SAK/L motif
F;210-222/Region: GTP-binding sAK/L motif
F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-134 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02592.1; PID:g16503449; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Staphylococcus aureus
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jul-2004
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50.0%; Pred. No. 36;
tive 3; Mismatches
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6.2;
           Mismatches
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Pred. No.
           3;
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                                                                  2 QTPQPLLQVMMEPQG 16
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-639 <NES>
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              7.
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AS6779
              Matches
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A;Cross-references: UNIPROT:P33567
R;Nakajo, S.; Tsukada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.
Bubmitted to JIPID, October 1993
A;Description: A new brain-specific 14-kDa protein is a phosphoprotein: Its complete ami
A;Reference number: JU0238
A;Accession: JU0238
A;Accession: JU0238
A;Molecule type: protein
A;Residues: 1-134 <NA2>
C;Keywords: brain
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: C96534
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
M.; Rooney, T.; Tulu, S.Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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J. Nourochem. 59, 1624-1629, 1992.
A;Title: Cloning and characterization of the cDNA encoding a novel brain-specific 14-kDa A;Reference number: 156498; MUID:93019240; PMID:1402909
A;Reference number: 156498
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C.Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoneuroprotein 14 - rat
C;Species: Nattus sp. (rat)
C;Date: 26-7ul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: IS6498
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A;Residues: 1-137 <RES>
A;Cross-references: GB:D17764; NID:g409780; PIDN:BAA04610.1; PID:g459235
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No.
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Pred. No.
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105 EPLIEPLMEPEGE 117
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105 EPLIEPLMEPEGE 117
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Best Local Similarity 46.2.
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Best Local Similarity 46.2
Matches 6; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-671 <STO>
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A; Gene: F14J22.3 C, Genetics:

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C;Accession: AE1406

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matlok, C.; Schlueter, T.; Simoes, N.; Tisterz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-695 <GLA>
A,Cross-references: UNIPROT:Q8Y421; GB:NC_003210; PIDN:CAD00867.1; PID:g16412154; GSPDB:C
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Cispecies: Comparative genomics of Listeria species:
A;Ritle: Comparative genomics of Listeria species:
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; Superfamily: translation elongation factor G; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.3%; Score 43; DB 40.0%; Pred. No. 39; ive 7; Mismatches
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Job time : 13.2091 secs
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                                                                                                                                                                                                                                                                                                                                     A; Accession: AE1406
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C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
R;Su, Y.A.; He, P.; Clewell, D.B.
Antimicrob. Agents Chemother. 36, 769-778, 1992
A;Title: Characterization of the tet(M) determinant of Tn916: evidence for regulation by A;Reterence number: A56779; MUD:92368175; PMID:1323953
A;Recension: A56779; MUD:92368175; PMID:1323953
A;Status: preliminary
A;Accession: A56779; MUD:92368175; PMID:1323953
A;Status: preliminary
A;Mocession: A56779; MUD:92368175; PMID:1318321; PIDN:AAA24784.1; PID:9148322
A;Notes: sequence extracted from NCBI backbone (NCBIN:111076, NCBIP:111078)
C;Superfamily: translation elongation factor G; translation elongation factor G; translation elongation factor G; translation elongation factor G; translation elongation factor Tu homology cETU>
C;Superfamily: translation elongation factor Tu homology cETU>
F;131/Domain: translation elongation factor Tu homology cETU>
F;121-131/Region: GTP-binding NKXD motif
F;1220-222/Region: GTP-binding SAK/L motif
F;126-131/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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51312
ctracycline resistance protein tetM - Enterococcus faecalis transposon Tn916
C; Species: Enterococcus faecalis
C; Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C; Accession: S13142
C; Accession: S13142
R; Burdett, V.
Nucleic Acids Res. 18, 6137, 1990
A; Title: Nucleotide sequence of the tet(M) gene of Tn916.
A; Reference number: S13142; MUID:91045089; PMID:2172929
A; Accession: S13142
A; Molecule type: DNA
A; Residues: 1-639 cBUR>
A; Accession: Using A; Residues: Using A; Residues: 1-639 cBUR>
A; Cross-references: UniPROT:P21598; EMBL:X56353; NID:g47061; PIDN:CAA39796.1; PID:g47062
A; Residues: 1-639 cBUR>
A; Title: Purification and characterization of Tet(M), a protein that renders ribosomes rancember: A; Reference number: A23749; MUID:9131580; PMID:1993661
A; Contents: annotation; function; amino end of purified recombinant protein
A; Note: protein purified after expression in E. coli shown to be ribosome-dependent GTPa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Gene: LetM
C;Superfamily: translation elongation factor G; translation elongation factor Tu homolog
C;Keywords: antibiotic resistence; GTP binding; nucleotide binding; P-loop
C;Keywords: antibiotic resistence; GTP binding; nucleotide binding motif A (P-loop)
F;10-131/Domain: translation elongation factor Tu homology <ETU>F;10-131/Region: nucleotide-binding motif A (P-loop)
F;128-131/Region: GTP-binding NKXD motif
F;200-222/Region: GTP-binding SAK/L motif
F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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Pred. No. 36;
3; Mismatches
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50.0%; Pred. No. 36;
ive 3; Mismatches
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IENPHPLLQTTVEP 352
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Best Local Similarity 50.0
Matches 7; Conservative
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Length 695

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A;Cross-references: UNIPROT:092715; GB:AL592022; PIDN:CAC98029.1; PID:g16415339; GSPDB:GN
A;Experimental source: strain Clip11262
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C,Superfamily: translation elongation factor G, translation elongation factor Tu homology
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                                                                                                                                                      48.3%; Score 43; DB 40.0%; Pred. No. 39; iive 7; Mismatches
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translation elongation factor G homolog fus [imported] - Listeria monocytogenes (strain C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                           1612378 segs, 512079187 residues
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SYUB BOVIN
SYUB HUMAN
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Q6CMX4
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Maximum Match 100%
Listing first 45 summaries
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Q89y61 bradyrhizob		Q8ta01 trypanosoma O9fxa2 arabidopsis			Q8ifi2 trypanosoma		Q7t5c7 cercopithec	Q805x6 cercopithec	Q7sah0 neurospora	Q633a0 bacillus ce	Q7m561 brachydanio
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ALIGNMENTS

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Frangeul

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.9%; Score 48; DB 1; Length 692;
40.0%; Pred. No. 35;
tive 8; Mismatches 1; Indels
   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Elongation factor G (EF-G)
Name=fusA; OrderedLocusNames=gbs1812;
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRANT=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Kusniok C., Buchrieser C., Chevalier F., Fran Madek T., Zouine M., Couve E., Lalioui L., Poyart C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GTP (By similarity).
85 GTP (By similarity).
138 GTP (By similarity).
76598 MW; 199DA941BC7F9182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0484; EF-G; 1.
TIGRFAMS; TIGRO0231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
Complete protecme; Elongation factor; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P13551; 1DAR.

Sagalist; gbs1812; -.

HAMAP; MF_00054; -; 1.

InterPro; 1PR004540; EF-G.

InterPro; 1PR000640; EFG C.

InterPro; 1PR00512; EFG III V.

InterPro; 1PR00517; EFG III V.

InterPro; 1PR00517; EFG III V.

InterPro; 1PR00517; EFG III V.

InterPro; 1PR00525; Small GTP.

InterPro; 1PR005000; Translat_factor.

Pfam; PF00679; EFG C; 1.

Pfam; PF00164; EFG C; 1.

Pfam; PF00169; GTP_EFTU; 1.
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400 IEVPEPVIQLMVEPK 414
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692 AA;
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                                                                                                                                                                                                                                       proteins.";
Submitted (NAY-2000) to Swiss-Prot.
-- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome (By similarity).
-- SUBCELLULAR LOCATION: Cytoplasmic.
-- SIMILARITY: Belongs to the GTP-binding elongation factor family.
                                                                                                                                                                  STRAIN=JRS4 / Serotype M6;
Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
VanBogelen R.A.;
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
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40.0%; Pred. No. 35;
tive 8; Mismatches 1; Indels
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84 GTP (By similarity).
137 GTP (By similarity).
76397 MW; DS9B857A2CDB40CD CRC64;
                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
                                                                                                                                                PARTIAL SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE006493, AAK33347.1; --
EMBL, AE014140, AAK78807.1; --
EMBL, AP005141; BAC63301.1; --
EMBL, AE009973; AAL97040.1; --
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Best Local Similarity 40.00,
                                                                                                                                                                                                                                                                                                                                                                       EF-G/EF-2 subfamily.
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691 AA;
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692 AA.

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EFG STRA3 Q8E3E7;

RESULT 2 EFG_STRA3

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                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391(1302).
-!- FUNCTION: This protein promotes the Grey-dependent translocation of the nascent protein chain from the A-site to the P-site of the
                                                                                                                                        STRAIN=2603 V/R / Serctype V;
STRAIN=2603 V/R / Serctype V;
STRAIN=2202988; Pubmed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; Pubmed=12200547; DOI=10.1073/pnas.182380799;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Ranaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 692;
Pred. No. 35;
                                                                             Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (By similarity).
GTP (By similarity).
GTP (By similarity).
36BCF199BA006AB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRPAMS; TIGRO0484; EF-G; 1.
TIGREAMS; TIGRO0231; small GTP; 1.
TROSITE; PS00301; EFACTOR GTP; 1.
Complete proteome; Elongation factor; GTP-binding; Procein blosynthesis.
             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Elongation factor G (EP-G)
Name-fusA, OrderedLocusNames-SAG1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Pred. ...
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InterPro; IPR004540; BF-G.
InterPro; IPR004540; BF-G.
InterPro; IPR009022; BFG III V.
InterPro; IPR005573; BFG IV.
InterPro; IPR005573; BFG IV.
InterPro; IPR004161; BFT<sup>U</sup> D2.
InterPro; IPR004161; BFT<sup>U</sup> D2.
InterPro; IPR005090; Translat_factor.
Pfam; PF00679; BFG C; 1.
Pfam; PF00109; GTP_ERTU; 1.
Pfam; PF010409; GTP_ERTU; 1.
Pfam; PF01015; BFG IV; 1.
Pfam; PF01015; BFG IV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE014272; AAN00632.1; -.
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Best Local Similarity 40.v-
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85
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692 AA;
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TIGR; SAG1769; -.
                                                                                                                    NCBI_TaxID=216466;
                                                                                                         Streptococcus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
-!- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-UAIS9 / ATCC 700610 / Serotype c;
MEDLINE=22255063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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GTP (By similarity).
GTP (By similarity).
5.252763A2606E5E04 CRC64;
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InterPro; PR004540; BF-G.

InterPro; PR000451; BF-G.

InterPro; PR0004021; BFG-G.

InterPro; PR000521; BFG-III V.

InterPro; PR000521; BFG-IV.

InterPro; PR0005225; Small GTP.

InterPro; PR000525; Small GTP.

InterPro; PR000595; BFG-G.

InterPro; PR000595; BFG-G.

InterPro; PR00059; BFG-G.

InterPro; PR00059; BFG-G.

InterPro; PR00059; BFG-G.

InterPro; PR00159; BFG-G.

In
                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Elongation factor G (EF-G).
     693 AA
                                                                                               10-OCT-2003 (Rel. 42, Created)
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     STANDARD;
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693 AA;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1309;
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EFG STRMU
QBDVV4;
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HAMAP; MF_00054; -; 1.
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709 AA;
                                                                          SEQUENCE FROM N.A.
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                NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                      ribosome.
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SEQUENCE
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Q928G4
             NAMES OF THE STREET OF THE STR
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STRAINSTANCE 5-3;

By Dubwed=14966310;

By Pitdet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barretto C., Apridmore R.D., Berger B., Cauvet M., Altermann E., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;

The genome sequence of the probiotic intestinal bacterium

Lactobacillus johnsonii NCC 533.", No. 101:2512-2517(2004).

R. Droc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

R. Embi, Aboly2201; Aso808323.1;

R. GO; GO:0000525; F:GTP binding; IEA.

R. GO; GO:00005412; P:protein biosynthesis; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

BY GO; GO:0006414; P:translational elongation; IEA.

DR InterPro; IPR000963; Bac Ig/alb_bind.

DR InterPro; IPR000640; EFG_III.V.

DR InterPro; IPR000615; EFG_III.V.

DR InterPro; IPR000195; ProtEyn_GTPbind.

DR InterPro; IPR000195; ProtEyn_GTPbind.

DR InterPro; IPR000195; ProtEyn_GTPbind.

DR InterPro; IPR000195; ProtEyn_GTPbind.

DR InterPro; IPR0001051; EFTU D.

DR InterPro; IPR0001051; EFTU D.

DR InterPro; IPR0001051; EFTU D.

DR InterPro; IPR0001051; FTU D.
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O9CDG1;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
55-JUL-2004 (Rel. 44, Last annotation update)
85-JUL-2004 (Rel. 46, Last annotation update)
105-JUL-2004 (Rel. 41, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
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Pfam; PF03764; EFG IV; 1.

Pfam; PF03764; EFG IV; 1.

Pfam; PF03164; EFG IV; 1.

Pfam; PF03164; EFTU D2; 1.

PRINTS; PR00315; ELONGATARCT.

TIGRFAMs; TIGR00484; EF-G; 1.

TIGRFAMs; TIGR00231; small GTP; 1.

PROSITE; PS030301; ER-GTOR GTP; 1.

COMPLETE proteome; Elongation factor; GTP-binding.

SEQUENCE 698 AA; 76916 MW; B73C135DEE5F8662 CRC64;
                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                 698 AA
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400 IEVPEPVIQLMVEPK 414
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1 LOTPOPLLQVMMEPQ 15
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Best Local Similarity 53.3.
Best Local 8; Conservative
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  longation factor G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=33959;
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Q74L90;
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MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.169701;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis spp. lactis IL1403.";
Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                             -!- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GTP (By similarity).
85 GTP (By similarity).
138 GTP (By similarity).
77955 MW; 1EAD29D65A748032 CRC64;
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INTERPRO, IPRO04401, BF.G.
INTERPRO, IPRO06401, BF.G.
INTERPRO, IPRO06401, BF.G.
INTERPRO, IPRO090221, BF.G.
INTERPRO, IPRO041611, BF.TŪ D2.
INTERPRO, IPRO040161, BF.TŪ D2.
INTERPRO, IPRO090001, Translat_factor.
Ff.am, PF006791, BF.G.C.
INTERPRO, IPRO090001, Translat_factor.
Ff.am, PF006791, BF.G.C.
INTERPRO, IPRO09001, Translat_factor.
Ff.am, PF000091, GTP_EFTU, 1.
Ff.am, PF001015, BF.G.VO, 1.
Ff.am, PF001161, GTP_EFTU, D2, 1.
Ff.am, PF001161, GTP_EFTU, D2, 1.
Ff.am, PF001161, BF.G.VOATNFCT.
INTERPAMS, TIGRO04841, BF.G.
INTERPAMS, TIGROO4841, BF.G.
INTERPAMS, TIGRO04841, BF.G.
INTERPAMS, TIGROO4841, BF.G.
INTERPAMS, TIGROO4841, BF.G.
INTERPAMS, TIGROO4841, BF.G.
INTERPAMS, TIGROO4841, BF.G.
INTERPROPERTOR OF THE BF.G.
INTERPROP
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006455; AAK06358.1; -.
PIR; D86907; D86907.
HSSP; P13551; 1DAR.
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01-DEC-2001 (TEMBLEEL. 19, C;
01-DEC-2001 (TEMBLEEL. 19, L;
01-JUN-2003 (TEMBLEEL. 24, L;
Lin2571 protein.
OrderedLocusNames=lin2571;
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415 IEVPEPVIQLMVEPK 429
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Best Local Similarity 40.00
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                 SEQUENCE FROM N.A.

C STRAIN=CLIP 11262 / Serovar Ga;

X MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;

A Glaser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chectouani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Britan K.-D., Fahih H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaeft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Matcournam A., Mata Vicente J., No B., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Comparative genomics of Listeria species.";

Science 294:849-852(2001)
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Gevers D., Danielsen M., Huys G., Swings J.;
"Molecular characterization of tet (M) genes in Lactobacillus isolates from different types of fermented dry sausage.";
Appl. Brviron. Microbiol. 69:1270-1275(2003).
-i- FUNCTION: Abolishes the inhibitory effect of tetracyclin on protein synthesis by a non-covalent modification of the ribosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
TetM/tetO subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus sakei subsp. sakei.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 192 Aa; 20841 MW; BEB4B4D3261DDA74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Tetracycline resistance protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IRRO00640; EFG C.
InterPro; IRRO09022; EFG III_V.
InterPro; IRRO04161; EFFG IV.
InterPro; IRRO04161; EFFG D2.
InterPro; IRRO04162; FrotSyn GTPbind.
InterPro; IRRO09120; TCR TetCOM.
InterPro; IRRO09000; Translat_factor.
Pfam; PP00679; EFG_C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listilist; LIN2571; -.
TIGRFAMS; TIGR01603; maj_tail_phil3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 TPKPLPGGVEISVEPQGD 48
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Matches 9; Conserv
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DOI=10.1128/ABS.69.2.1201.2203.3

Molecular characterization of tet(M) genes in Lactobacillus isolates

"Molecular characterization of tet(M) genes

"In From Torion Microbiol. 69:1270-1275 (2003).

"In Appl. Environ. Microbiol. 69:1270-1275 (2003).

"In Appl. Environ. Microbiol. 69:1270-1275 (2003).

"In Promission Synthesis by a non-covalent modification of the ribosomes

(By similarity).

"TetM/tetC subfamily.

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Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU D2; 1.
PRINTS; PR01037; TGRTETOM.
Antibiotic resistance; Cyclin; GTP-binding; Protein biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactobacillus sakei subsp. carnosus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                      473 473 473 473 EBA66C29002820EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                    51.7%; Score 46; DB 2;
llarity 50.0%; Pred. No. 50;
Conservative 4; Mismatches 3
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01-JUN-2003 (TrEMBLrel. 24, Last sequence
01-MAR-2004 (TrEMBLrel. 26, Last annotatio
Tetracycline resistance protein (Fragment)
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InterPro; IPR000795; ProtSyn GTPbind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR002127, TCR TetOOM.
InterPro, IPR009000, Translat_factor.
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InterPro; IPR009022; EFG_III_V.
InterPro; IPR005517; EFG_IV.
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Pfam; PF03764; EFG_IV; 1.
Pfam; PF00009; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
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246 IENPHPLLQITVEP 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
7; Conserva
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Best Local Similarity
7; Conserve
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NCBI_TaxID=214325;

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C -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.

C Tenk/tecto subfamily.

E REMB.; AY149590; AAN84494.;

R GO; GO:0005525; F:GTP binding; IEA.

R GO; GO:00034612; F:ranslation elongation factor activity; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R GO; GO:0006412; P:response to antibiotic; IEA.

R InterPro; IPR0009022; EFG IV.

R InterPro; IPR0004161; EFG IV.

R InterPro; IPR0004161; EFG IV.

R InterPro; IPR0004161; EPG IV.

R InterPro; IPR0004161; EPG IV.

R InterPro; IPR000127; TCR_TetOQW.

InterPro; IPR000127; TCR_TetOQW.

InterPro; IPR000127; TCR_TetOQW.
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Gevers D., Danielsen M., Huye G., Swings J.;
Gevers D., Danielsen M., Huye G., Swings J.;
"Molecular characterization of tet(M) genes in Lactobacillus isolates
from different types of fermented dry sausage.";
Appl. Environ. Microbiol. 69:1270-1275(2003).
-1- FUNCTION: Abolishes the inhibitory effect of tetracyclin on
protein. synthesis by a non-covalent modification of the ribosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tetracycline resistance protein (Fragment).
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26, Last annotation update)
                                                                                                                                                                                                                   474 AA
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence v
01-MR-2004 (TrEMBLrel. 26, Last annotation
Tetracycline resistance protein (Fragment).
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                                                                                                                                                                                                                   PRT;
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MEDLINE=22458139; PubMed=12571056;
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Pfam; PF03764; BFG_IV; 1.
Pfam; PF00009; GTP_EFTU_D: 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
246 IENPHPLLQITVEP 259
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246 IENPHPLLQITVEP 259
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nes 7; Conservative
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus plantarum.
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Q84GV1
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Gaps
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GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003746; F:translation elongation factor activity; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
GO; GO:0046677; P:response to antibiotic; IEA.
GO; GO:0006414; P:rranslational elongation; IEA.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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                                                                                                                                                                                                                                                                                                                         InterPro; IPR000640; EFG II. V.
InterPro; IPR000640; EFG III. V.
InterPro; IPR0004161; EFG IV.
InterPro; IPR0004161; EFTG IV.
InterPro; IPR000127; FCR TetOQM.
InterPro; IPR000127; TCR TetOQM.
InterPro; IPR000100; Translat_factor.
Pfam; PP00009; EFG C; I.
Pfam; PP00009; GTP_EFTU; I.
Pfam; PP001099; GTP_EFTU; I.
Pfam; PP010109; TCR EFTU 2; I.
Pfam; PP010109; TCR EFTU 2; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 AA;
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Matches
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PRINTS; PR01037; TČRTETÕQM.
Antibiotic resistance; Cyclin; GTP-binding; Protein biosynthesis.
                                                                                                                                  Query Match 51.7%; Score 46; DB 2; Best Local Similarity 50.0%; Pred. No. 51; Matches 7; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                   477 AA.
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                                                                                                                                                                                                                                                                                                                                                   PRT;
 Pfam; PF03144; GTP_EFTU_D2; 1.
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249 IENPHPLLQITVEP 262
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248 IENPHPLLQITVEP 261
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Best Local Similarity
'... Queserve
                                                                                                   475 AA;
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SEQUENCE
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MEDLINE=22458139; PubMed=12571056;
MEDLINE=22458139; PubMed=12571056;
MEDLINE=22458139; PubMed=1275.2003;
BOI=10.1128/AEM.69.2.1270-1275.2003;
Gevers D., Danielsen M., Huys G., Swings J.;
"Molecular characterization of tet(M) genes in Lactobacillus isolates from different types of fermented dry sausage.";
Appl. Environ. Microbiol. 69:1270-1275(2003).
-1- FUNCTION: Abolishes the inhibitory effect of tetracyclin on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein synthesis by a non-covalent modification of the ribosomes (By similarity).

-!-SINILARTIY: Belongs to the GTP-binding elongation factor family. TetM/tetO subNamily.

EMBL; AX149581; AbNaM485.1; -. GO; GO:0005525; F:GTP binding; IEA.

GO; GO:000525; F:GTP binding; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006414; P:response to antibiotic; IEA.

GO; GO:0006414; P:translational elongation; IEA.
GO; GO:0005525; F:GTP binding; IEA.

GO; GO:000746; F:translation elongation factor activity; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:006414; P:response to antibiotic; IEA.

GO; GO:006414; P:translational elongation; IEA.

R InterPro; IPRO00640; EPG_C.

R InterPro; IPRO00602; EPG_II V.

INTERPRO; IPRO00602; EPG_II V.

R InterPro; IPRO0121; EPG_IV.

R InterPro; IPRO0121; EPG_IV.

R InterPro; IPRO0121; TCR_TetCOM.

R InterPro; IPRO01217; TCR_TetCOM.

R InterPro; IPRO0120; Translat_factor.

Pfam; PF00170; TERC_C: 1.

Pfam; PF00170; TERC_C: 1.

R Pfam; PF00174; GTP_EFTU; 1.

R Pfam; PF00174; GTP_EFTU; 1.

R Pfam; PF00174; GTP_EFTU; 1.

R Pfam; PF00174; TCR_TETCOM.

M Antibiotic resistance; Cyclin; GTP-binding; Protein biosynthesis.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxIb=214325;
                                                                                                                                                                                                                                                                                                                                                                                        475 AA; 54163 MW; AB4FF5EC84F7D570 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tetracycline resistance protein (Fragment).
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251 IENPHPLLQITVEP 264
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AC 0845W
AC 0845W
DT 01-JUJ
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MEDITRE-22458139; PubMed=12571056; MEDITRE-22458139; PubMed=12571056; DOI=10.1128/AEM.69.2.1270-1275.2003; Gevera D., Danielsen M., Huys G., Swings J.; Dolecular characterization of tet(M) genes in Lactobacillus isolates from different types of fermented dry sausage."; Appl. Environ. Microbiol. 69:1270-1275.2003).

-!- FUNCTION: Abolishes the inhibitory effect of tetracyclin on protein synthesis by a non-covalent modification of the ribosomes (By similarity).

-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
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R InterPro; IPR000622; EFG_III_V.
R InterPro; IPR000522; EFG_III_V.
R InterPro; IPR000517; EFG_IV.
R InterPro; IPR000161; EFTG_IV.
R InterPro; IPR000161; EFTG_IV.
R InterPro; IPR000161; Translat_factor.
R InterPro; IPR000900; Translat_factor.
R Pfam; PF000679; EFG_IV.
R Pfam; PF00144; EFG_IV.
R Pfam; PF00144; EFG_IV.
R Pfam; PF00144; GTP_EFTU. 1.
R Pfam; PF001617; TGREETOOM.
R Antibiotic resistance; Cyclin; GTP-binding; Protein biosynthesis.
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EMBL; A149578; A3M84482.1; -

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0003746; F:translation elongation factor activity; IEA.

GO; GO:0004612; P:presponse to antibiotic; IEA.

GO; GO:00046677; P:response to antibiotic; IEA.

GO; GO:0006414; F:translational elongation; IEA.
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                                                                        Length 475;
                                                                                                                                             3; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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54190 MW; CDE3197026C272E0 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tetracycline resistance protein (Fragment).
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DOI=10.1128/AEM.69.2.1270-1275.2003;
Gevers D., Danielsen M., Huys G., Swings J.;
George D., Danielsen M., Huys G., Swings J.;
"Molecular characterization of tet (M) genes in Lactobacillus isolates from different types of fermented dry sausage.";
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-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
TetM/tetO subfamily.
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R GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0064412; P:protein biosynthesis; IEA.

GO; GO:006441; P:response to antibiotic; IEA.

GO; GO:006441; P:response to antibiotic; IEA.

GO; GO:006441; P:response to antibiotic; IEA.

InterPro; IPR00512; EFG_III_V.

R InterPro; IPR00512; EFG_III_V.

R InterPro; IPR00512; FFG_III_V.

R InterPro; IPR0010795; ProtSyn GrPbind.

R InterPro; IPR0010795; ProtSyn GrPbind.

R Pfam; PF00679; EFG_C; 1.

R Pfam; PF00679; EFG_C; 1.

R Pfam; PF00009; GTP_EFTU, 1.

R Pfam; PF001099; GTP_EFTU, 1.
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Lactobacillus sakei subsp. carnosus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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477 AA; 54376 MW; 4DDED454C4D22EBB CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tetracycline resistance protein (Fragment).
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AAUSSO15 ABMS1534 AAW64933 AAW45073 AAY45072 AAY20811 AABC3292 AABC3292 AABC3293 AABC3293 AABC3293 AABC3316 AABC3317	ABG09426 ADH09924 ADH09922 ADH09923 ADL83154 ADPS4647 ADP24002
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ALIGNMENTS

Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient .. 0 Length 18 Indels Dermatological; oxidative stress regulator; colostrinin. 100.0%; Score 98; DB 4; I 100.0%; Pred. No. 3.7e-07; tive 0; Mismatches 0; Boldogh I; Ž Claim 6; Page 25; 48pp; English. AAB72502 standard; peptide; 18 17-AUG-2000; 2000WO-US022665. 99US-0149310P. entry) (TEXA) UNIV TEXAS SYSTEM Query Match 100. Best Local Similarity 100. Matches 18; Conservative Stanton GJ, Hughes TK, Colostrinin peptide #3 WPI; 2001-218342/22.

Gaps

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AAB59325;

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a proline rich polypeptide aggregate confained in colostrum. The peptides bave immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing cytokines production, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders of the central nervous system, neurological disorders, mental disorders, dementia, neurodegenerative diseases, and that all actions and disorders of the immune system, bacterial and viral infections and acquired immunological deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
    dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroprotective; neural cell differentiation regulator; colostrinin;
                                                                                                                                                                                                                                                                                                                                                                                         Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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Pred. No. 3.7e-07;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 34; 50pp; English.
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(REGE-) REGEN THERAPEUTICS PLC.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                Hughes TK,
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                          infection
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                                                                                                   WO200111937-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                Stanton GJ,
                                                                                                                                         22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulator.
                        neurosis;
                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                                        Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
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                                                                                                                                   AAB59325 standard; peptide; 18
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DOPPDVEKPDLQPFQVQS 18
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Matches 18; Conserv
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AAB72248;

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method for promoting cell differentiation (e.g. neural cell differentiation). The method involves contacting cells with a neural cell regulator (i.e. a colostrinin peptide) in order to change the cells in morphology to form neural cells. Colostrinin is a proline-rich polypeptide aggregate that is present in colostrum. The method of the
                                                               Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                              The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                   cell differentiation; neural cell regulator; colostrinin peptide; cell formation; proline-rich polypeptide aggregate; colostrum; cell treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoting cell differentiation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
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                                                                                                                                                                                                                                                                                                                                                                                                 Neural cell regulatory colostrinin peptide 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boldogh I, Stanton JG, Hughes TK;
                                                                                                                                                                                                                                                                                                                               AA014579 standard; peptide; 18 AA
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                                                                                                           Claim 6; Page 21; 35pp; English.
                                                                                                                                                                                                                                                     1 DOPPDVEKPDLOPFOVOS 18
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                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Marches 18; Conservative
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(TEXA ) UNIV TEXAS SYSTEM
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                                            WPI; 2001-226545/23.
                                                                                                                                                                                      Sequence 18 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                     Boldogh I;
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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell requlator in claimed methods of the invention. It is classified as having a crequistor in claimed methods of the invention. It is classified as having a cytokine in a cell by contact with an immunological regulator, where the cytokine in a cell by contact with an immunological regulator, where the coll is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions effective to induce a cytokine; modulating an immune response in a patient by administering an immunological regulator under conditions effective to induce a cytokine; where the immunological regulator is caministered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibod cells with a blood cell regulator; where the blood cells are consecting consecting consecting consecting consecting consecting an immune remammalian or human, and and where the blood cells are increased in number or differentiated; and a
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cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colostrinin constituent peptide.
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(REGE-) REGEN THERAPEUTICS PLC.
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organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide

regeneration, and replacement of cells, tissues and

enhanced repair,

Sequence 18 AA;

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                                                                                                                                                                                                                                                                                                                       Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
         cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10. It was one of the best overall inducers in almost all cytokine and blood cell proliferation experiments conducted
modulating blood cell proliferation in a patent. A claimed
                                                                                                                                   Gaps
                                                                                                                                  ;
0
                                                                                                             Length 18;
                                                                                                 Score 98; DB 5; Lengtn Lo. Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Optionally C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boldogh I;
                                                                                                                                                                                                                                                                                                 Colostrinin constituent peptide #3.
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                                                                                                                                                                 100.0%;
                                                                                                                                                       18
                                                                                                                                                                                                                                AAE20230 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-2000; 2000WO-US022776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-2000; 2000WO-US022776.
                                                                                                                                                      1 DOPPDVEKPDLOPFOVOS
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                        Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes TK,
                                                                                      Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200213850-A1
                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                             18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanton GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2002
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                                                                                                                                                                                                             RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colostrinin for e.g. modulating an intracellular signaling
ile in a cell, down regulating 4HNE-mediated lipid peroxidation in
inhibiting apoptosis in a cell, or protecting against DNA damage i
                                                                                                                                                                                                                                                                                                         modulator; colostrinin; intracellular signaling molecule modulator; 4HNB-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor; 4HNB-protein adduct formation reduction; 4HNB-mediated glutathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
                                         Gaps
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgiades JA, Hughes TK,
100.0%; Score 98; DB 5; 100.0%; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                               Constituent peptide of colostrinin SEQ ID NO:3.
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; SEQ ID NO 3; 46pp; English.
                                                                                                                                                                                  AA.
                                       ;0
                                                                                                                                                                                ADN60297 standard; peptide; 18
                                                                     18
                                                                                         DOPPDVEXPDLOPFOVOS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2003; 2003WO-US033423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2002; 2002US-0420369P
                                                                       1 DOPPDVEKPDLQPFQVQS
                                                                                                                                                                                                                                              29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIV TEXAS SYSTEM.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOLDOGH I.
STANTON J G.
GEORGIADES J A.
HUGHES T K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanton JG,
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                        Similarity
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    Query Match
Best Local Simi]
Matches 18; (
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                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                ADN60297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEXA)
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a cell.
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                                                                                                                                                                   ADN60297
                                                                                                                                                   RESULT
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regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level analogue. The invention is used for modulating the oxidative stress level corps. The invention is used for modulating the oxidative stress level corps. Or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/ after patient. Firth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stress results in

Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.

WPI; 2002-269151/31.

The invention relates to a composition which comprises a blood cell

6; Page 25; 51pp; English.

Claim

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a peptide that can be recovered from ovine colostrinin using the method of the invention. The invention provides a method for the recovery of peptides (especially colostrinin) from colostrum in substantially pure, biologically active form and in high yield. The method involves mixing the colostrum with an alcohol to form an alcohol phase containing the colostrinin and a precipitate containing higher molecular weight caseins and other proteins. Best results are obtained using methanol or ethanol of at least 80% and preferably up to 100%, purity. The alcohol phase is then separated from the precipitate, and the colostrinin is separated from the alcohol, preferably by evaporation, to form a colostrinin-rich phase, which is recovered. A precipitation agent, such as ammonium sulfate, may be added to induce precipitation of the colostrinin peptides. The method is generally applicable to the separation of peptides from fluids containing higher molecular weight proteins, lipids, carbohydrates and/or nucleic
                                                                                                                                                                                                              ö
Colostrinin, or its constituent peptide or active analogue is useful for inhibiting apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                ö
                                                                                                                                                                     100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 3.7e-07;
                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colostrum; colostrinin; sheep; peptide purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kruzel ML;
                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polanowski A, Wilusz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 18; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       ADS74401 standard; peptide; 18 AA
                                                                                                                                                                                                                                                       1 DQPPDVEKPDLQPFQVQS 18
                                                                                                                                                                                                                                                                             DOPPDVEKPDLOPFQVQS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-2004; 2004WO-GB001014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2003; 2003GB-00005552.
08-MAR-2004; 2004GB-00005190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovine colostrinin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recovering alcohol phase.
                                                                                                                                                                                                              18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-677519/66.
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004081038-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgiades JA,
                                                                                                                              Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS74401;
                                                                                                                                                                       Query Match
                                                                                                                                                                                             Local
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RESULT 9

ADS74401

DY ADS74401

DY ADS74401

DY ADS7401

DY ADS74

Sequence 18 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheep, colostrinin, proline rich polypeptide, colostrum, immune disorder, central nervous system disorder, dietary supplement, beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a distary supplement, and to promote the dissolution of beta-amyloid plaques
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100.0%; Score 98; DB 8; Length 18; 100.0%; Pred. No. 3.7e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Ewe colostrinin peptide fragment derived sequence #15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                AABS9355 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOPPDVEKPDLOPFOVOS 19
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                                                                                                 18
                                                                                                                                             DOPPDVEKPDLOPFOVOS 18
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Conservative (
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                                                                                               1 DQPPDVEKPDLQPFQVQS
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    Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by amyloid plaques.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georgiades JA;
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                                                                                                                                                                                                                                                                                                               AAB59355;
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ABU28927
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Enterococcus faecalis infection; transcription regulatory element;

Enterococcus faecalis,

US6617156-B1

09-SEP-2003.

Zyskind JW; Xu HH;

antibacterial

98US-00134000 97US-0055778P

Bush D;

WPI; 2003-895394/82. Doucette-Stamm LA,

N-PSDB; ADH83796

(DOUC/) DOUCETTE-STAMM L A.

15-AUG-1997; 13-AUG-1998;

BUSH D.

(BUSH/)

screening

Enterococcus faecalis polypeptide #1681

(first entry)

22-APR-2004

ADH87201;

ADH87201 standard; protein; 1056 AA.

ADH87201

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us-10-691-330-3.rag

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the invention fractive to an isolated muchael actd comparising any one or the invention fractive to an inspecification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contained to polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular compound that influences the activity of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway or equired for the proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiting a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to. isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids

C required for proliferation to. isolate candidate molecules for rational required for proliferation and proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation as a serventy and the remaining the proposed and the remaining the required for proliferation as a servent servent servent servent servent servent sequences or a servent or an antional search and a servent servent servent servent servent sequences are servent sequences
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                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
  Protein encoded by Prokaryotic essential gene #14454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 56851; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                        2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELIT-) ELITRA PHARM INC.
                                                                                                      Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029926/02
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                                                                                                                                                     WO200277183-A2
                                                                                                                                                                                                                                                                                                        21-MAR-2001;
                                                                                                                                                                                                    03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang Wall
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New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.

Disclosure; SEQ ID NO 5086; 193pp; English.

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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in the polynucleotides can be used to detect the presence of E. faecalis in diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein useful for treating neurological disease Seq 1962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51, DB 7; Length 105
Pred. No. 1.4e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR08456 standard; protein; 116 AA.
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47.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1056 AA;
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Gaps

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Length 1056;

human; oligo-capping method; diagnostic marker; gene therapy;

|||||::||: ||:: 256 DQPVDLQKPETKQFQLK 272

Ouery Match
Best Local Similarity 47.1.
Best Local Similarity 67.1.

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ID AAM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to molecules and the encoded proteins thereof. Specifically, it refers to come are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as attribodies, antibodies, antib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense er motor function; emoctoral reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein modification and maintenance molecule, PMMM, cytostatic, antiarteriosclerotic, anticonvulgant, nootropic, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T, Isono Y, Sugiyama T,
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PMMM protein amino acid sequence SeqID12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 8
Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1962; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ71952 standard; protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.0%;
                                                                                                                                                                                                                                                                                                  12-FEB-2004; 2004EP-00003145.
                                                                                                                                                                                                                                                                                                                                              14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
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Wakamatsu A, Ishii S,
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tes 8; Conserv
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                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                 EP1447413-A2
                                                                                                    tranquiliser
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This invention relates to novel protein modification and maintenance molecules (PMMM) and polymucleotides which identify and encode PMMM. The invention may be useful for the development of compositions with a cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, antiallergic, antimicrobial, antiinflammatory, endocrine-Gen or thyromimetic activity. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of PMMM, such as cell proliferative (for example cancer, atherosclerosis), neurological (for example pilepsy, Huntington's disease, stroke), immune/inflammatory (for example AIDS, allergies) and developmental (for example Hypothyroidism, Cushing's syndrome) disorders, or infections. These are also useful in assessing the effects of exagenous compounds on the expression of nucleic acid and amino acid sequences of PMMM. The present sequence is that of a human PMMM protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human protein modification and maintenance molecules (PMVM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMVM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nguyen DB;
Tribouley CM;
antinflammatory; endocrine-Gen; thyromimetic; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; ALDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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R, Chawla NK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2002; 2002US-0398143P.
09-AUG-2002; 2002US-0402458P.
12-AUG-2002; 2002US-0403289P.
27-AUG-2002; 2002US-0409354P.
06-SEP-2002; 2002US-0409354P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2003; 2003WO-US023249
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                               WO2004009797-A2
                                                                                                                                                                                                                                                                                      Homo sapiens.
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Interpretation in the treatment of the polymental control activity elating to cytokine, cell proliferation or cell differentiation or which may induce cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polymeptides have various cytokine-like activities, e.g. seem cell growth factor activity, immunomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, archritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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, Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xv
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 4066-4067; 6221pp; English
                                                                    Human protein SEQ ID NO 1730,
                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-0059322.
30-NOV-2000; 2000US-0058422.
                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                        2000US-00496914
                                                                                                                                                                                                                                                                                                                                                       2000US-00560875.
                                   (first entry)
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                                                                                                                                                                                                                                WO200157190-A2
                                                                                                                                                                                             Homo sapiens.
                               06-NOV-2001
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20-JUN-2000;
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AAM79068;
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Query Match 49.0%; Score 48; DB 4; Length 377; Best Local Similarity 72.7%; Pred. No. 1.2e+02; Matches 8; Conservative 1; Mismatches 2; Indels

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Gaps ö

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13, Appl
37365, A
52582, A
15435, A
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5086, Ap
4389, Ap
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                                                                   April 12, 2005, 07:49:30 ; Search time 21.1091 Seconds (without alignments) 63.654 Million cell updates/sec
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Sequence 1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-134-000C-5086

US-09-134-000C-3089

US-09-744-128-16

US-09-744-128-16

US-09-406-711-13

US-09-806-132-13

US-09-270-76-52582

US-09-270-76-52582

US-09-270-76-15435

US-09-157-021-31

US-09-157-021-31

US-09-157-021-31

US-09-591-514-31

US-09-694-519-1

US-09-694-519-1

US-09-694-519-1

US-09-032-365A-8

US-09-032-365A-8
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
                                                                                                               US-10-691-330-3
98
1 DQPPDVEKPDLQPFQVQS 18
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Gapop 10.0 , Gapext 0:5
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Maximum DB.seq length: 200000000
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Match Length DB
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        28
        42
        42.9
        506
        3
        US-09-032-365A-62
        Sequence 62, Appli 30.09-032-365A-62

        29
        42
        42.9
        506
        3
        US-08-018-01-8
        Sequence 4, Appli 31.05-09-018-01

        31
        42
        42.9
        506
        3
        US-08-955-918C-10
        Sequence 10, Appli 32.05-03

        33
        42
        42.9
        506
        3
        US-08-955-918C-10
        Sequence 10, Appli 32.05-03

        34
        42
        42.9
        506
        4
        US-09-032-365A-0
        Sequence 60, Appli 32.05-03

        35
        42
        42.9
        518
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        US-09-032-365A-0
        Sequence 58, Appli 32.05-03

        36
        42
        42.9
        561
        1
        US-09-032-365A-0
        Sequence 57, Appli 32.05-03

        36
        42
        42.9
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        1
        US-09-032-365A-10
        Sequence 57, Appli 32.05-03

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        42
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        US-09-032-365A-10
        Sequence 57, Appli 32.05-03

        37
        42
        42.9
        564
        4
        US-09-032-365A-10
        Sequence 22.589, Appli 32.05-03
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ALIGNMENTS

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105 PPSAQQPFQQPFQPQA 120
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        3 PPDVEKPDLQPFQVQS 18
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Best Local Similarity 57.1%;
Matches 8; Conservative
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ORGANISM: Unknown Organism
                                                                                                      RESULT 5
US-09-744-128-16
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US-09-880-132-13
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4389
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APPLICANT: Veis et al.

TITLE OF INVENTION:

FILE REFERENCE: 27636/36983

CURRENT APPLICATION NUMBER: US/09/744,128

CURRENT FILING DATE: 2001-05-16

PRIOR PILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN 3.1

SEQ ID NO 17
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                                                                                                                      Query Match 52.0%; Score 51; DB 4; Length 1056; Best Local Similarity 47.1%; Pred. No. 16; Matches 8; Conservative 6; Mismatches 3; Indels
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16;
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46.9%; Score 46; DB 4; Length 180;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels
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Patent No. 6677306
SEQ ID NO 5086
LENGTH: 1056
TYPE: PRT
ORGANISM: Enterococcus faecalis
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265 DQPVDLQKPETKQFQLK 281
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ORGANISM: Artificial sequence
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Matches 10; Conservative
                                                                                 US-09-134-000C-5086
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US-07-792-600-31
  LENGTH: 118
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                                                          APPLICANT: Kenten, John
APPLICANT: Kenten, John
APPLICANT: Roberts, Steven
TITLE OP INVENTION: CONTROLLING PROTEIN LEVELS IN EUCARYOTIC ORGANISMS
FILE REFERENCE: 275-6
CURRENT APPLICATION NUMBER: US/09/880,132
CURRENT PILING DATE: 2001-06-14
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SSOTUMARE: Patentin Ver. 2.1
SSOTUMARE: Patentin Ver. 2.1
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Sequence 52582, Application US/09270767

Sequence 52582, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-270-767-37365

Sequence 37365, Application US/09270767

Sequence 37365, Application US/09270767

Sequence 37365, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

PILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 37365

LENGTH: 118
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2.2;
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Pred. No.
Application US/09880132
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 57.1%;
Matches 8; Conservative
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23 QPVDITKADLKQPFQ 37
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 10; Conservative
                    Patent No. 6559280
GENERAL INFORMATION:
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Sequence 15435, Application US/09248796A

Patent No. 6747130

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NOTEEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-06-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15435
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APPLICANT: WANG, TERESA S.-F.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter G. Carroll
STREET: 220 Montgomery Street, Suite 710
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
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                                                                                             DB 4; Length 118;
                                                                                                                                         Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SÖFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,600
                                                                                             Score 44.5; DE
Pred. No. 14;
1; Mismatches
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TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-270-767-52582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 QPPQLEPPVLEP-QVSS 378
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                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                       2 QPPDVEKPDL-QPFQ 15
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ATTORNEY/AGENT INFORMATION:
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ORGANISM: Candida albicans
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Matches 10; Conservative
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MEDIUM TYPE: Floppy
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US-09-631-603-23
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US-09-156-842-31
is Sequence 31, Application US/09156842A
is Sequence 31, Application US/09156842A
is Patent No. 6103473
is GENERAL INFORMATION:
is APPLICANT: Wang, Teresa S. F.
it TILE OF INVENTION: DATE: 1998-09-18
is FILE REFERENCE: STDU-0348E
is CURRENT APPLICATION NUMBER: US/09/156,842A
is CURRENT FILING DATE: 1998-09-18
is EARLIER FILING DATE: 1991-11-15
is SOFTWARE: PATENT ONCS: 35
is SOFTWARE: PATENT ONCS: 35
is SEQ ID NO 31
it LENGTH: 1462
it TYPE: PRT
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APPLICANT: Copeland, William C.
TITLE OF INVENTION: Drug Design Assay
TITLE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/157,021A
CURRENT FILING DATE: 1998-09-18
EARLIER FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 1462
RECISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: STDU-00097
FELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAX: (415) 397-8338
FELEFAX: (415) 397-8338
FENGTH: 1462 amino acids
FYPE: AMINO ACID
FYPE: A
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255 DEPMEVEEVDLEPMAAKA 272
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US-09-157-021-31
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Best Local Similarity
Matches 7; Conserva
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APPLICANT: Lloyd, Clare
APPLICANT: Weich, Natin R.
TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
TITLE OF INVENTION: Secretin-like Family and Uses Thereof
FILE REFERENCE: 5800-48A
CURRENT APPLICATION NUMBER: 09/515,781
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/515,781
PRIOR PLILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/146,916
PRIOR APPLICATION NUMBER: 60/146,916
PRIOR PRIOR SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 457
                                                            Gaps
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       Length 1462;
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43.9%; Score 43; DB 4; Length 1462;
Best Local Similarity 38.9%; Pred. No. 3.7e+02;
Matches 7; Conservative 6; Mismatches 5; Indels
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Pred. No. 1.5e+02;
3; Mismatches 4; Indels
     Score 43; DB 3; I
Pred. No. 3.7e+02;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TILLE OF INVENTION: Drug Design Assay
FILE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/591,514
CURRENT APPLICATION NUMBER: US/09/157,021
PRIOR APPLICATION NUMBER: US/09/157,021
PRIOR RILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
SPIOR FILING DATE: 1998-09-18
SPIOR FILING DATE: 1998-09-18
SPIOR PRIOR PRIOR DATE: 1998-09-18
SOFTWARE: PARENTING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PARENTIN VET. 2.0
SEQ ID NO 31
LENGTH: 1462
                                                                                                                                                                                                                          RESULT 14
US-09-591-514-31
; Sequence 31, Application US/09591514
; Patent No. 6670161
; Patent No. 6870161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09631603
Patent No. 6733990
GENERAL INFORMATION:
                                                                                                                                      |:| :||: ||:|
255 DEPMEVEEVDLEPMAAKA 272
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                                                                                                      1 DOPPDVEKPDLOPFQVQS 18
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Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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324 RPPDIRKSDSSPY 336
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Best Local Similarity 46.2
Matches 6; Conservative
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US-09-591-514-31
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Search completed: April 12, 2005, 08:07:50 Job time: 22.1091 secs

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Sequence 56851, App Sequence 118, App Sequence 10746, A Sequence 204178, Sequence 200861, Sequence 233789, Sequence 13, App1 Sequence 13, App1 Sequence 13, App1
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Sequence 3, Appli
                                                                                                                                                                     April 12, 2005, 07:49:30 ; Search time 55.8 Seconds (without alignments) 107.096 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: \( cgn2 \frac{6}\) ptodata/1/pubpaa/PCT \text{NEW DUB.pep:*} \)

2: \( cgn2 \frac{6}\) ptodata/1/pubpaa/PCT \text{NEW PUB.pep:*} \)

3: \( cgn2 \frac{6}\) ptodata/1/pubpaa/PCT \text{NEW PUB.pep:*} \)

4: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOG \text{NEW PUB.pep:*} \)

5: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOG \text{NEW PUB.pep:*} \)

6: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{NEW PUB.pep:*} \)

7: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{NEW PUB.pep:*} \)

8: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{NEW PUB.pep:*} \)

9: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{NEW PUB.pep:*} \)

10: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{PUBCOMB.pep:*} \)

11: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{PUBCOMB.pep:*} \)

12: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{PUBCOMB.pep:*} \)

13: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{PUBCOMB.pep:*} \)

14: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USOB \text{PUBCOMB.pep:*} \)

15: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USIOB \text{PUBCOMB.pep:*} \)

16: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USIOB \text{PUBCOMB.pep:*} \)

17: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USIOB \text{PUBCOMB.pep:*} \)

18: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USIOB \text{PUBCOMB.pep:*} \)

19: \( cgn2 \frac{6}\) ptodata/1/pubpaa/USIOB \text{PUB.pep:*} \)

10: \( cgn2 \frac{6}\) ptoda
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-10-691-330-3

5 US-10-2122A-56851

5 US-10-210-130-118

6 US-02-815-242-10746

6 US-10-437-963-200661

6 US-10-437-963-200661

6 US-10-425-114-39945

5 US-10-425-114-39945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-149-13
US-09-880-132-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                              US-10-691-330-3
98
1 DQPPDVEKPDLQPFQVQS 18
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Maximum DB
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Sequence 766, App Sequence 165, App Sequence 157119, Sequence 114326, Sequence 4, Appli Sequence 4, Appli Sequence 1577, Ap Sequence 39967, A Sequence 39967, A Sequence 118548, Sequence 54044, A Sequence 118548, Sequence 57, Ap Sequence 54044, A Sequence 54044, A Sequence 54044, A Sequence 54059, Appli Sequence 706, Appli Se Sequence 1831, Ap Sequence 41207, A Sequence 409, App Sequence 409, App Sequence 133514, Sequence 579, App Sequence 679, App Sequence 618, App Sequence 43.5

ALIGNMENTS

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Sequence 3, Application US/10281652;
Sequence 3, Application US/10281652;
Publication No. US20030091606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: UNMBER: US/10/281,652
CURRENT APPLICATION NUMBER: US/09/641,803
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATEULIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Best Local Similarity
Matches 18; Conserv
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LENGTH: 18
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Gaps
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFWARE: PatentIn version 3.1
LENGTH: 1047
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APPLICANT: Catterton, Elina
APPLICANT: Shenoy, Suresh G.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 15; Length 1047;
Pred. No. 1.1e+02;
6; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, Application US/10210130 Publication No. US20040014053A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spytek, Kimberly A.
Gerlach, Valerie
Burgess, Catherine E.
Khramtsov, Nikolai V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boldog, Ferenc L.
Padigaru, Muralidhara
Smithson, Glennda
                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-56851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 DQPVDLQKPETKQFQLK 272
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Shimkets, Richard A
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Gorman, Linda
Vernet, Corine A.M.
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Chaudhuri, Amitabha
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47.1%;
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Guo, Xiaojia Sasha
Anderson, David W.
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Spaderna, Steven K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zerhusen, Bryan D. APPLICANT: Patturajan, Meera APPLICANT: Kekuda, Ramesh APPLICANT: Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rieger, Daniel K.
Pena, Carol E.A.
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Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ort, Tatiana
Ellerman, Karen
Rastelli, Luca
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Gangolli, Esha A
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Ooi, Chean Eng
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Best Local Similarity
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Berghs,
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                                                      Sequence 3. Application US/10691330

Publication No. US20050042300A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beldogh, Istvan
APPLICANT: Georgiades, Jerzy A.
APPLICANT: Georgiades, Jerzy A.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Georgiades, Jerzy A.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Georgiades, Jerzy A.
APPLICANT: GEORGIAGES, Jerzy A.
APPLICANT: HILEROR K. Jr.
APPLICANT: GEORGIAGES, Jerzy A.
APPLICANT: Marian
TITLE OF INVENTION: THEREOR AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
CURRENT TLING DATE: 2003-10-22
CURRENT APPLICATION NUMBER: US/10/691,330
CURRENT APPLICATION NUMBER: US/10/691,330
FRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 18
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0348

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 05/11,078

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PRIOR PILING DATE: 2000-09-05

PRIOR PILING DATE: 2000-09-05

PRIOR PILING DATE: 2000-09-05

PRIOR PILING DATE: 2000-09-03

PRIOR PILING DATE: 2000-09-03

PRIOR PILING DATE: 2000-09-03

PRIOR PILING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 98; DB 17; Length 18; Best Local Similarity 100.0%; Pred. No. 3.3e-07; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56851, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Synthetic Peptides
US-10-691-330-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQPPDVEKPDLQPFQVQS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-282-122A-56851
                                                 US-10-691-330-3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 15; Length 377;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tranic, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 2001-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/204, 848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 9; I
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                               SEQ ID NO 1
1 LENGTH: 377
   TYPE: PRT
   TYGANISM: Home sapiens
   FEATURE:
   NAME/KEY: misc_feature
   JOHER INFORMATION: Incyte ID No: 5566074CD1
US-10-250-613-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-204178
; Sequence 204178, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10746, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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US-09-815-242-10746
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Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 PPDVEQPQTOP 371
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                       SOFTWARE: PERL Program
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CURRENT APPLICATION NUMBER: US/10/210,130
CURRENT APPLICATION NUMBER: US/10/210,130
CURRENT PILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR PILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PELING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-13
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APPLICANT: YAO, Monique G.; DING, Li,
APPLICANT: YAO, Monique G.; DING, Li,
APPLICANT: HONCHELL, Cynthia D.; YUE, Henry;
APPLICANT: TANG, Y. Tom; WARREN, Bridget A.;
APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
APPLICANT: ISON, Craig H.; AZIMZAI, Yalda;
APPLICANT: LAL, Preeti G.; SANJANWALA, Madhusudan M.;
APPLICANT: ELLIOTT, VICAS, S.
TITLE OF INVENTION: CYTOSKELETAL-ASSOCIATED PROTEINS
FILE REFERENCE: PF-0878 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 15;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: PCT/USO2/00178
PRIOR APPLICATION NUMBER: US 60/260,085
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 60/269,111
PRIOR PILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 36
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Publication No. US20040096828A1
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361 PPDVEQPQTQP 371
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-210-130-118
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ORGANISM:
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Sequence 233789, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREMENTS: 32-1(52233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233789
LENGTH: 336
                           APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Cao, Yongwei
TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NOWER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 52231
LENGTH: 313
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. OTHER INFORMATION: Clone ID: PAT_MRT3847_53136C.1.pep US-10-424-599-233789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.9%; Score 46; DB 15; Best Local Similarity 53.3%; Pred. No. 1.6e+02; Matches 8; Conservative 4; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700894460_FLI.pep
US-10-425-114-52231
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 QPVELEEPNQQPLQV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ::|:|: || || 149 QPVELEEPNQQPLQV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 OPPDVEKPDLOPFOV 16
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                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
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US-10-424-599-233789
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Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Avoid K.

APPLICANT: Avoid K.

APPLICANT: Avoid K.

APPLICANT: Avoid K.

APPLICANT: Barbazuk, Brad

APPLICANT: Buckharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38 -21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 200861
                                                                                                                         APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping Parplicant Li, Ping Parplicant Li, Ping Reperior Li, Ping Reperior Li Cor Invention: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 204178

LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_99291C.1.pep
US-10-437-963-204178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96290C.1.pep
US-10-437-963-200861
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Publication No. US20040034B8BA1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                         Wu, Wei
Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 OPPDVEKPDLOPFOVOS 18
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La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||||
15 PPDVEKPD 22
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US-10-425-114-52231
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SEQ ID NO 13
LENGTH: 26
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; Sequence 13, Application US/09880149
; Patent No. US20020146843A1
; GENERAL INFORMATION:
    APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TILLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUCARYOTIC ORGANISMS
; FILE REFERENCE: 2757-5
; CURRENT APPLICATION NUMBER: US/09/880,149
; CURRENT PILING DATE: 1999-08-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR PILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-880-132-13
US-09-880-132-13
Sequence 13, Application US/09880132
Patent No. US20020173049A1
GENERAL INFORMATION:
APPLICANT: Renten, John
APPLICANT: Roberts, Steven
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2757-6
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                   Length 337;
                                                                                                                                                                                                                                                 Score 46; DB 15; Length 33
Pred. No. 1.7e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 9; Length 26;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels.
                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 700904208_FLI.pep
US-10-425-114-39945
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CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/406,781
PRIOR FILING DATE: 1999-09-28
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39945
LENGTH: 337
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VET: 2.1
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                2 QPPDVEKPDLQPFQV 16
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PPGVEEPDVGPLPV 15
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Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown Organism
                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-880-149-13
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Sequence 228647, Application US/10424599
; Sequence 228647, Application US/10424599
; Sequence 228647, Application US/2040031072A1
; Sequence 228647, Application No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION UNDRER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kenten, John
APPLICANT: Kenten, John
TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUCARYOTIC ORGANISMS
TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUCARYOTIC ORGANISMS
FILE REFERENCE: 2757-6
CURRENT APPLICATION NUMBER: US/10/345,281
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/880,132
PRIOR APPLICATION NUMBER: 09/406,781
PRIOR APPLICATION NUMBER: 60/19,81
PRIOR PELING DATE: 1999-02-8
PRIOR PELING DATE: 1999-02-8
PRIOR PELING DATE: 1999-02-8
PRIOR PILING DATE: 1999-02-8
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 13
SEQ ID NO 13
                                                                                                                                                                                                                                                                        Gaps
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                                                                                         ) OTHER INFORMATION: Description of Unknown Organism: PEST example ; OTHER INFORMATION: sequence US-09-880-132-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
COTHER INFORMATION: Description of Unknown Organism: PEST example
COTHER INFORMATION: sequence
US-10-345-281-13
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Best Local Similarity 57.1%; Pred, No. 16; Length 26;
Matches 8; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                          Query Match
45.9%; Score 45; DB 9;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-345-281-13
; Sequence 13, Application US/10345281
; Publication No. US20030153727A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  3 PPDVEKPDLQPFQV 16
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TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
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) ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48496C.1.pep
US-10-424-599-228647
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0; Gaps Query Match
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels

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S DVEKPDLQPFQV 16 ||:|||::||: |45 DVKKPDVKPVQI 156 . В

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Search completed: April 12, 2005, 07:55:20 Job time : 55.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                              OM protein - protein search, using sw model
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April 12, 2005, 07:49:31 ; Search time 85.4182 Seconds Run on:

(without alignments)
107.909 Million cell updates/sec

US-10-691-330-3 98 1 DQPPDVEKPDLQPFQVQS 18 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	caulobacter	bordetella	bordetella	bordetella	enterococcu	enterococcu	homo sapien	bos taurus	enterococcu	yarrowia li	ustilago ma				ustilago ma	symbiobacte				streptomyce	mus musculu	mus sp a	agrobacteri	agrobacteri	oryza sativ	mus musculu	rattus norv			ustilago ma	drosophila
		Q9a5s4	Q7w511	07wgh6	03×60	088168	Q832p0	08ng68	P27117	Q835m9	06ch19	Q700g4	0100ge	0700g8	010010	099118	067qh0	Q9c8m8	Q9c8m9	Q84r17	09x818	Q9d2d5	09qw43	08nep8	Q7cye5	Oeedw0	P63277	P63278	Q6pcw7	Q700k9	Q700h9	097539
SOPPERATES	ID	Q9A5S4	Q7W511	O7WGH6	039X6Q	088168	Q832P0	TTL HUMAN	DCOR BOVIN	Q835 <u>M</u> 9	беснгэ	Q700G4	Q700G6	Q700G8	Q70019	099118	0670но	Q9C8M8	Q9C8M9	Q84R17	Q9X8L8	Q9D2D5	Q9QW43	QBUEBB	Q7CYES	QEEQWO	AMEX_MOUSE	AMEX_RAT	Q6PCW7	Q700K9	0100Н9	09V539
	DB	. ~	7	~	~	~	~	М	H	7	~	~	~	N	~	~	7	~	~	N	~	~	~	~	~	~	н	-	~	~	~	~
	Length	483	182	182	182	392	1047	377	461	541	652	320	320	320	320	404	467	516	719	126	134	137	141	187	199	202	210	210	219	318	320	499
de	Query Match Length	56.1	52.0	52.0	52.0	52.0	52.0	49.0	49.0	49.0	49.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	47.4	•	•	46.9	•	•	46.9	46.9	46.9	46.9	46.9	46.9	46.9
	Score	55	51	51	51	51	51	48	48	48	48	47	47	47	47	47	47	47	47	46.5	46	46	46	46	46	46	46	46	46	46	46	46
	Result No.	-	7	9	4	2	9	7	8	6	10	11	. 12	13	14	15	16	17	18	19		21	22	23	24	25	56	27	28	53	30	31

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01-077-2003 (TrEMBLrel. 25, Created) 01-077-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

182 AA.

PRT;

PRELIMINARY;

Q7W511; Q7W511

22555

RESULT 2 Q7W511

O7zxg8 xenopus lae O6imn2 xenopus lae O7515 xenopus lae O7515 xenopus lae O7515 xenopus lae O7515 xenopus lae O8mmf4 drosophila O7512 glatdia lam O88326 mesocricetu O7373 gallus gall O7373 gallus gall O75546 homo sapien O8bht7 mus musculu O6zqf1 mus musculu	
Q7ZXG8 Q6IMN2 C6IMN2 SUB2 DEIRA Q8MMF4 Q8MMF4 Q8C6H1 Q8C6H1 Y258 HUMAN Q8BHT7 Q6ZQF1 Q6ZQF1 Q6ZQF1	
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627 6680 728 728 1424 1424 1345 369 369 391 391 391 570	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
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## ALIGNMENTS

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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; bubmed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE-21173698; bubmed=11259647; DOI=10.1073/pnas.061029298;

Nicrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

POCOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004494; F:methylmalonyl-CoA mutase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPror, IFRO06099; MMCOA_mutase.
Pfam; PFO1642; MM_COA_mutase; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AE005906; AAK24344.1; -.
PIR; D87543; D87543.
HSSP; P11652; IREQ.
TIGR; CC2373; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 AA; 50032 MW; 194F84D33268D6D5 CRC64;
                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Methylmalonyl-CoA mutase, beta subunit.
OrderedLocusNames=CC2373;
 483 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||:|| || 439 DKPPEVETPDSSAFAVQ 455
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hes 10; Conservative
PRELIMINARY;
                                                                                                                                 Caulobacter crescentus
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Q9A5S4
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Matches
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us-10-691-330-3.rup

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Complete proteome.
SEQUENCE 182 AA;
                                                                                          Query Match
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Q9X6Z0;
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                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

X MEDLINE=22827954; PubMed-12910271; DOI=10.1038/Mg1227;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Gerdeno-Tarraga A.M., Temple L., James K.D., Harris B., Quail M.A.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Baron N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Baron N., Cherevach I.,

RA Achtman M., Atkin B., Steron S., Basham D., Baris B., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Genet. 35:32-40(2003).

RE EMBL; Exception and Bordetella bronchiseptica.";

RT Gool 2019867; Couter membrane; IEA.

PRE PRESSERVENT TERRON7460: Smah Omla.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE_25827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE_25827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M. T.G., Churcher C.M., Bentley S.D., Mungall K.L., A Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Akin R., Baker S., Basham D., Bason N., Cherevach I., A Chillingworth T., Collins M., Cromin A., Davis P., Doggett J., A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis, Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Outer membrane lipoprotein.
Name=omlA; OrderedLocusNames=BPP3495;
Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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Name-omla, OrderedlocusNames-BB3943;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 51; DB 2; Length 182; 72.7%; Pred. No. 9.5; 0; Indels ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007450; SmpA_OmlA.
Pfam, PF04355; SmpA_OmlA; 1.
Complete proteome; Lipoprotein.
SEQUENCE 182 AA; 20490 MW; 73F6DB9B1714377F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BX640449; CAE34306.1; -. GQ; GO; C0019867; C:outer membrane; IEA. InterPro; IPR001450; SmpA_OmlA. Pfan; PF04355; SmpA_OmlA. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.7,,
Best Local Similarity 72.7,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||||||:
114 EQPDLQPFQIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 EKPDLOPFOVO 17
                                                                                                                                     NCBI TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7WGH6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7WGH6
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STRAIN=Tohamm I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cordeno-Tarraga A. -M., Temple L., James K.D., Harris B., Quall M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Achtman M., Atkin R., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Sauders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

T. Bordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella pertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                    52.0%; Score 51; DB 2; Length 182; 72.7%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 51; DB 2; Length 182; 72.7%; Pred. No. 9.5; 0; Indels ive 3; Mismatches 0; Indels
                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prade1 E.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
20504 MW; DCF6DB9B17142113 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73F6DB9B171AD791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
02-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Outer membrane lipoprotein.
Name=OmlA, Synonyms=OmlA, OrderedLocusNames=BP2508,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 AA.
                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Genet. 35:32-40(2003).

EMBL; AJ238308; CAB41013.1; -.

EMBL; BX640418; CAE42780.1; -.

GO, GO:0019867; C:outer membrane; IEA.

InterPro; IPR007450; SmpA_OmlA.
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF04355; SmpA OmlA; 1.
Complete proteome; Lipoprotein.
SEQUENCE 182 AA; 20489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Query Match
Best Local Similarity 72...,
Best Local Similarity 72...,
                                                                              Local Similarity 72.7
hes 8; Conservative
                                                                                                                                                                                                  114 EQPDLQPFQIE 124
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                               7 EKPDLQPFQVQ 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 EKPDLQPFQVQ 17
182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=TohamaI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=520;
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MEDINEE 223825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINEE 223825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E., Bronstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Araba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahon D.K., Muzny D.M., Soderjern E.J., Lu X., Gibbs R.A., Piby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkedley R.W., Touchman J.W., Green E.D., Dickson M.C., Abramson M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Bonerzth A., Schein J.B., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + detyrosinated alpha-tubulin + L-tyrosine = alpha-tubulin + ADP + phosphate. -!- COFACTOR: Magnesium and potassium (By similarity). -!- SUBUNIT: Monomer (By similarity). -!- SUBUNITY: Contains 1 TTL domain.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Miyazaki K., Okamoto Y., Kato C., Sakamoto M., Ohira M., Morohashi A.,
Nakagawara A.;
Nakagawara tubulin tyrosine ligase mRNA, complete cds.";
"Homo sapiens tubulin tyrosine ligase mRNA, complete cds.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lauber J., Bahr A., Mewes H.-W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (UN-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the posttranslarional addition of a tyrosine to the C-terminal end of detyrosinated alpha-tubulin (By
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                           Q8NG68; Q72302; Q8N426; Created)
05-UIL-2004 (Rel. 44, Created)
05-UIL-2004 (Rel. 44, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
Tubulin-tyrosine ligase (EC 6.3.2.25) (TTL).
377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro, IPR004344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB071393, BAC06832.2; -. EMBL, BC036819; AAH36819.1; -. EMBL, BX538316; CAD98091.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 205-377 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligase; Magnesium; Potassium.
DOMAIN 81 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:21586; TTL.
                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                      Name=TTL;
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                                                                                                                                                                                                                                                                                    EnterCoccus idecairs Osine...;
Infect. Immun. 66:413-423 (1998).
EMBL; AF071085; AAC35928.1; -.
EMBL; AF071085; Researching in the company of the company of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613; Paulsen I.T., Baneriel L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosyl transferase, group 2 family protein.
OrderedLocusNames=EF7181;
Entercoccus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes; Lactobacillales; Entercoccus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
   Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                  Xu Y., Murray B.E., Weinstock G.M.;
"A cluster of genes involved in polysaccharide biosynthesis from Enterococcus faecalis OGIRF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%; Score 51; DB 2; Length 1047; 47.1%; Pred. No. 63; 3; Indels ive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 51; DB 2; Length 392; ilarity 47.1%; Pred. No. 22; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1047 AA; 119728 MW; 621F8B792F814E36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1047 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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InterPro; IPR001601; Methyltransf.
InterPro; IPR001601; SAM bind.
Pfam, PF00515; Glycos transf 2: 1.
Complete protecome; Transferase.
SEQUENCE 1047 AA; 119728 MW; 623
                                                                                                                                                                MEDLINE=98380380; PubMed=9712783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| |::||: ||::
256 DQPVDLQKPETKQFQLK 272
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256 DQPVDLQKPETKQFQLK 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DQPPDVEKPDLQPFQVQ 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 47.1%;
8; Conservative
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STRAIN=V583 / ATCC 700802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                   SEQUENCE FROM N.A
                              NCBI_TaxID=1351;
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                                                                                                                                     STRAIN=OG1RF
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Q832P0

ઠ 셤 RESULT 6
093220
1D 098321
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001-

I -> V (in Ref. 3).

CONFLICT

RESULT 7 TTL_HUMAN

Matches

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424 DFPPGVEEPDVGPLPV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=EF1348;
                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 ('01-JUN-2003 ('01-OCT-2003 ('01-OCT-200) ('01-OCT-200) ('01-OCT-200) ('01-OCT-200) ('01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6CHL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                              RESULT 9
Q835M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26CHL9
                                                        셤
                                                                                                                                                                                                                                                                                                            DTT DDT LANGUS DD DT LANGUS DD DT LANGUS DD DT LANGUS DD DT LANGUS DD BENN LANGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9599316; PubMed=7774801; Yao J., Zadworny D., Kuhnlein U., Hayes J.F.; Molecular cloning of a bovine ornithine decarboxylase cDNA and its use in the detection of restriction fragment length polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity,
Phosphoserine (by CK2) (By similarity)
4E609B643E3B68FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the Orn/Lys/Arg decarboxylase class-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
-I- COFACTOR: Pyridoxal phosphate.
-I- PATHWAY: Polyamine biosynthesis; first (rate-limiting) step.
-I- SUBUNIT: Homodianer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyridoxal phosphate (By similarity)
                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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PROSITE; PS00879; ODR DC 2 1; 1.
PROSITE; PS00879; ODR DC 2 2; 1.
Decarboxylase; Lyase; Phosphorylation; Polyamine biosynthesis;
                                                                              DB 1; Length 377; 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 1; Length 461;
Pred. No. 75;
2; Mismatches 5; Indels
                                                                                                                                                                     2; Indels
    7A13E2C28E1AD6EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Normithine decarboxylase (EC 4.1.1.17) (ODC).
Bos taurus (Bovine).
                                                                                  Score 48; DB 1
Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00143; Decarbxylse2.
InterPro; IPR002433; Orn decarbxylse.
InterPro; IPR009006; Racem decarbox_C.
Pfam; PF02784; Orn_DAP_Arg_deC N; I.
Pfam; PF00278; Orn_DAP_Arg_deC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
43212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Holstein; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51345 MW;
                                                                     49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U36394; AAA79849.1; -.
EMBL; U18531; AAA86696.1; -.
HSSP; P11926; 1D7K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.0%;
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                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 56.2
9; Conservative
                                                                                                                                                                                                                                                                                               361 PPDVEQPQTQP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holsteins.";
Genome 38:325-331(1995).
                                                                                                                                                                                                                                                   3 PPDVEXPDLQP 13
377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyridoxal phosphate
                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOVIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
MOD_RES
SEQUENCE
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Best Local S
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
DCOR_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCOR P27117
                                                                                                                                                            Matches
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DQPPDVEKPDLQPFQV 16

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MEDITRE-2250857; PubMede-12663927; DOI=10.1126/science.1080613; Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fourts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J. Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A., Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=YAL10A07557g;
Yarrowia lipolytica CL1B99.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 AA; 62718 MW; ED0DB68653A7DC98 CRC64;
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004556; F:alpha-amylase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA.
541 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.0%; Score 48; DB 62.5%; Pred. No. 89; ive 1; Mismatches
                                                                                                              Glucan 1,6-alpha-glucosidase, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp amyl_cat_sub.
Pfam; PF00128; Alpha-amyl_ase; 1.
SWART; SM00642; Aamy; 1.
Complete proteome.
                                            (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last seq
(TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis.";
Science 299:2071-2074 (2003).
EMBL; AEO16951; AAO81139:1; --
HSSP; P21332; 1UOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 DOOPGKEKWDLOPMEV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DOPPDVEKPDLOPFOV 16
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les 10; Conservative
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=V583 / ATCC 700802;
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SOR REPRESENTATION OF THE STATE OF THE STATE

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Kaemper J.T., Friedrich M.W., Kahmann R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
1- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AJ30078; CAR34012.1. -
GO; GO:0005634; C:mucleus; IRA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                        Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 320 320
SEQUENCE 320 AA; 36137 MW; 227986FF213D4E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Homeodomain transcription factor BW6a (Fragment).
                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Homeodomain transcription factor BW6b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.0%; Score 47; DB 2; 47.1%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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Pfam; PF000046; Homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SWART; SW0389; HOX; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; HOMEOBOX 2; 1.
NNA-binding; Homeobox; Nuclear protein.
NON_TER 320 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                       (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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217 EPTDSTQPDLSPFRSES 233
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                                                                                                                                                                                                Ustilago maydis (Smut fungus)
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Best Local Similarity 47.13
Matches 8; Conservative
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     PRELIMINARY;
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SEQUENCE FROM N.A.
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05-JUL-2004
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0700G8
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Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Handraye F., Kachouri R., Handraye F., Kachouri R., Kerrest A., Kosull R., Lemire M., Joyet P., Kachouri R., Nicard J., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Semnene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Seniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Bouchier C., Caudran B., Scarpelli C., Gaillardin C., Weissenbach J., "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaemper J.T., Friedrich M.W., Kahmann R.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AJ630080; CAR34016.1; --
GO; GO:000536; C:nucleus; IEA.
GO; GO:0007700; F:transcription factor activity; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00136; Homeobox.
InterPro; IPR009057; Homeodomain_like.
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Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=5270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.0%; Score 48; DB 2; Length 652;
53.8%; Pred. No. 1.1e+02;
Live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 652 AA; 74732 MW; 7C20193BD6CDE435 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Homeodomain transcription factor BWGc (Fragment).
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PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
SMOSTE; PS5071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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217 EPTDSTQPDLSPFRSES 233
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Best Local Similarity 47.1%;
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169 DGPPELERPELDP 181
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MEDLINE=92154679; PubMed=1739973; DOI=10.1016/0092-8674(92)90141-X;
Gallilssen B., Bergemann J., Sandmann C., Schroeer B., Boelker M.,
Kahmann R.;
                                                                                                                                                                                                                                                                                                                                                                                Natural Leader (MAR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
I- SUBGELLULAR LOCATION: Nuclear (By similarity).
EMBL; AJ630067; CAR33909.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
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Eukaryota; Fungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=5270;
                         48.0%; Score 47; DB 2; Length 320; illarity 47.1%; Pred. No. 71; Conservative 4; Mismatches 5; Indels
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320 AA; 36049 MW; AOEFF383413E735A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Homeodomain transcription factor BW11 (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM0389; HOX; 1.
PROSITE; PS5071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TER 320 320
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Name=bW4;
                                        Best Local Similarity
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two-component regulatory system for self/non-self recognition in
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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SEQUENCE 404 AA; 45439 MW; 4B2C71857AC82910 CRC64;
                               Cell 68:647-657(1992).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; M84181; AAA34223.1; -.
PIR; D42094; D42094.
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47.1%; Pred. No. 92;
ative 4; Mismatches
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Prodom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE, PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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InterPro; IPR009057; Homeodomain_like.
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                                                                                                                 April 12, 2005, 07:49:31 ; Search time 67.2 Seconds (without alignments) 69.064 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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ABM68047 ABO60912 ABB91909 AAA53600 AAA53500 AAA53599 ABB91016 ADN73819 AABB91071 AAA53598 AAB8741 AAA53598 AAB8741 AAA535598 AAB8741 AAA535598 ABM741 AABM74174	ABU12454 ADJ28480 AAW88536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinii, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations.
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100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                     Dermatological; oxidative stress regulator; colostrinin.
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                             Boldogh I;
                                                                            AAB72503 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 25; 48pp; English
                                                                                                                                                                                                                                                                                                                                 17-AUG-2000; 2000WO-US022665.
                                                                                                                                                                                                                                                                                                                                                                99US-0149310P
                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                            (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                        Colostrinin peptide #4
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                                                                                                                                                                                                                                    Unidentified
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                                                                                                           AAB72503;
                                               RESULT 1
                                                               AAB72503
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AAB59323;

AAB59323

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Sequences AAB72246 - AAB72255 represent peptides derived from clostrinin, a proline rich polypeptide aggregate contained in colostrum. The peptides have immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing cytokines production, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders, dementia, neurodegenerative diseases, Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic disorders of the immune system, bacterial and viral infections and
neurodegenerative disease; Alzheimer's disease; psychosis;
infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuroprotective; neural cell differentiation regulator; colostrinin;
                                                                                                                                                                                                                                                                                                                                                                                    Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 4; Length 12; 100.0%; Pred. No. 0.00054; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  Georgiades J;
                                                                                                                                                                                                                                                                                                                  Boldogh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB72535 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.
(REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                  17-AUG-2000; 2000WO-US022818.
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Best Local Similarity 100.0%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colostrinin peptide
                                                                                                         WO200111937-A2.
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                                                                                                                                                                                                                                                                                                                Stanton GJ,
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             dementia; neurosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulator.
                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                      Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 4; I 100.0%; Pred. No. 0.00054;
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                                                                                                                                                                                                                                                   Ewe colostrinin peptide fragment B-8.
                                                                                                                                     AAB59323 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-00012852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1999;
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AAB72249;

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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell consisted methods of the invention. It is classified as having a beta-casein homologue precursor. Methods are claimed for: inducing a cabitation or an organism, and cell is present in a cell culture, a tissue, an organ or an organism, and the cell is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions a cell by contact with the immunological regulator under conditions a cell by contact with the immunological regulator under conditions a deflective to induce a cytokine, where the immunological regulator are sponse in a caministered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting antibody response; modulating blood cell proliferation by contacting antibody response; modulating blood cell regulator, where the blood cells are considered and are mammalian or human, and where the blood cells are increased in number or differentiated; and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colostrinin, colostrum, immunomodulator, cardiovascular,
blood cell regulator, cytokine inducer, beta-casein, human.
                                                                                                                                                         Length 12;
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                                                                                                                                                         100.0%; Score 62; DB 5; I 100.0%; Pred. No. 0.00054; ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              AAM51039 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colostrinin constituent peptide.
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                                                                                                                                                                                                                                                                               Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-269150/31
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Matches 12; Conserv
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Modified-site
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                                                                                                            use ot colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                                                                                                                                                       The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin end peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell differentiation; neural cell regulator; colostrinin peptide; cell formation; proline-rich polypeptide aggregate; colostrum; cell treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                             Claim 6; Page 21; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12 AA;
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Modified-site

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Neural neural neural

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March March

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The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, corgan, or organism; or for treating oxidative stress during/ after a premature birth or normal birth, preventing/delaying aging in a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or in the cell, such he same conditions when the oxidative stress results in regulator is not present. The modulation of oxidative stress results in chanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and
                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; oxigan; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
               cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
modulating blood cell proliferation in a patent. A claimed
                                                                                                                                                                                          Gaps
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                                                                                                                                                    Length 12;
                                                                                                                                                                                        0; Indels
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                                                                                                                                              100.0%; Score 62; DB 5; L
100.0%; Pred. No. 0.00054;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boldogh I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colostrinin constituent peptide #4.
                                                                                                                                                                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 25; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                            AAE20231 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-2000; 2000WO-US022776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US022776
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                           1 LFFFLPVVNVLP 12
                                                                                                                                                                                                                                                 Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-269151/31.
                                                                                                                                                              Best Local Similarity Matches 12: Conser
                                                                                                              Sequence 12 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the use of a modulator selected from colostrinin, its constituent peptide, its active analogue, and a combination of these, for modulating an intracellular sipaling molecule in a cell, down regulating 4HRE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, protecting against DNA damage in a cell, inhibiting apoptosis in a cell, protecting against DNA damage in a cell, and reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The modulator has cytostatic activity, and can be used as a 4HNE inhibitor. The modulator is useful in the manufacture of a medicament for reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated all adduct formation, inhibiting 4HNE-mediated activation of c-Jun MHZ-terminal kinases colostrinin, or its constituent peptide or active analogue is useful for inhibiting apoptosis in a cell, protecting against DNA damage in a cell,
                                                                                                                                                                                                                                                                                                                                                                                                                   modulator; colostrinin; intracellular signaling molecule modulator; 4HNB-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNB inhibitor; 4HNB-protein adduct formation reduction; 4HNB-mediated glucathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
such organs for .
The present
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                                                                                                                                 Indels
external organs), as well as enhanced preservation of stransplantation, implantation, or scientific research. sequence is a colostrinin constituent peptide
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                                                                                                Score 62; DB 5; L
Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                                                                     Constituent peptide of colostrinin SEQ ID NO:4.
                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 4; 46pp; English.
                                                                                                                                                                                                                                                                                   ADN60298 standard; peptide; 12 AA.
                                                                                                  100.08;
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                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004 (first entry)
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                                                                                                                                 Conservative
                                                                                                                                                                                        LFFFLPVVNVLP 12
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STANTON J G.
GEORGIADES J A.
HUGHES T K.
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                                                                                              Query Match
Best Local Similarity
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                                                                Sequence 12 AA;
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Sequence 12 AA;
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                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a peptide that can be recovered from covine colostrinin using the method of the invention. The invention covine colostrinin using the method of the invention. The invention corporates a method for the recovery of peptides (especially colostrinin) corporates a method involves mixing the colostrum with an alcohol to high yield. The method involves mixing the colostrum with an alcohol to containing higher molecular weight caseins and other proteins. Best containing higher molecular weight caseins and other proteins. Best creatists are obtained using methanol or channol of at least 80%, and preferably up to 100%, purity. The alcohol phase is then separated from the precipitate, and the colostrinin is separated from the alcohol, preferably by evaporation, to form a colostrinin-rich phase, which is recovered. A precipitation agent, such as ammonium sulfate, may be added either to the alcohol phase or, preferably, to the colostrinin-rich phase corporation of the colostrinin peptides. The method is containing induce precipitation of the colostrinin peptides. The method is containing to precipitation of the colostrinin peptides from fluids containing containing induce precipitation of the colostrinin peptides from fluids containing containing induce precipitation of the colostrinin peptides from fluids containing containing acide. In an example from the invention, the antigenic profile of acide. In an example from the invention, the antigenic profile of soft peptides was determined by ELISA using antibodies prepared against 9 synthetic peptides, including a peptide having the present sequence contains and periods antigen class B-9).
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or reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and recovering alcohol phase.
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                                                                                                                                 Length 12;
                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kruzel ML;
                                                                                                                             Score 62; DB 8; I
Pred. No. 0.00054;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polanowski A, Wilusz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 16; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                          ADS74399 standard; peptide; 12 AA.
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                                                                                                                                 100.0%;
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2004GB-00005190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovine colostrinin peptide
                                                                                                                                                                             12; Conservative
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                                                                                                                                                                                                                                               1 LFFFLPVVNVLP
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                                                                                                                                 Query Match
Best Local Similarity
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                                                                                        Sequence 12 AA;
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08-MAR-2004;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beca-amyloid plaques
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Length 12;
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100.0%; Score 62; DB 8; I
100.0%; Pred. No. 0.00054;
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                                                Mismatches
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                                                                                                                                                                                                                                                                                    AAB59353 standard; peptide; 14 AA.
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                  Local Similarity
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nes 12; Conserv
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         18 - JUN - 1999;
22 - JUN - 1999;
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24 - JUN - 1999;
28 - JUN - 1999;
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30 - JUL - 1999;
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31 - J
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28-UUL-1999;
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11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
14-AUG-1999;
15-AUG-1999;
16-AUG-1999;
           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                               Arabidopsis thaliana protein fragment SEQ ID NO: 40711
                                                                                                                                                                                                                                                                              990S-0121825P.
990S-0123180P.
990S-012548P.
990S-01264P.
990S-01264B.
990S-0127462P.
990S-0130845P.
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990S-013248P.
990S-013428P.
990S-013458P.
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99US-0139463P.
99US-0139750P.
18-OCT-2000 (first entry)
                                                                                                                                     Arabidopsis thaliana
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05-MAR-1999;
23-MAR-1999;
23-MAR-1999;
24-MAR-1999;
06-APR-1999;
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16-APR-1999;
16-APR-1999;
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32-APR-1999;
32-APR-1999;
33-APR-1999;
34-APR-1999;
35-APR-1999;
36-APR-1999;
36-APR-1PR-1PR-1PR
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18-JUN-1999;
18-JUN-1999;
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990S-0121825P

990S-0123180P

990S-012578BP

990S-0126264P

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990S-0127462P

990S-0128234P

990S-0130610P

990S-0130610P

990S-0132484P

990S-0134768P

990S-013421P

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990S-0139460P

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990S-0139460P

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990S-0139460P
                                                                    25-FEB-2000; 2000EP-00301439
           Arabidopsis thaliana.
                              EP1033405-A2
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990S-0151066P

990S-0151030P

990S-0151303P

990S-0151430P

990S-015363P

990S-015363P

990S-0154039P

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990S-01609P
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99US-0161405P.
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Matches 7; Conservative
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135 YFFLPVINXL 144
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01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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AAG33578
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990S-0140991P.
990S-0141287P.
990S-0142184P.
990S-0142184P.
990S-0142055P.
990S-0142039P.
990S-0144339P.
990S-0144334P.
990S-0144332P.
990S-014538P.
990S-0147303P.
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990S-0147303P.
990S-0147333P.
990S-014932P.
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990S-014992P.
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99US-0152363P.
99US-0153070P.
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16-AUG-1999;
17-AUG-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 40709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG33577 standard; protein; 221 AA
990S-0153758P.
990S-0154018P.
990S-0154739P.
990S-0155139P.
990S-0155486P.
990S-0155486P.
990S-0156458P.
990S-0156458P.
990S-015753P.
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990S-015753P.
990S-015923P.
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990S-015923P.
990S-015933P.
990S-016983P.
990S-0160814P.
990S-016081P.
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13-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
26-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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06-SEP-2000.

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12-JUL-1999; 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999;	16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;	19-JUL-1999; 19-JUL-1999; 19-JUL-1999;	20-JUL-1999; 20-JUL-1999;	20-JUL-1999; 21-JUL-1999; 21-JUL-1999;	21-JUL-1999; 22-JUL-1999; 22-JUL-1999;	22-JUL-1999; 22-JUL-1999; 23-JUL-1999;	23-JUL-1999; 23-JUL-1999; 26-JUL-1999;	27-JUL-1999; 27-JUL-1999; 27-JUL-1999;	28-JUL-1999; 02-AUG-1999;	02-AUG-1999; 02-AUG-1999;	03-AUG-1999; 04-AUG-1999; 04-AUG-1999;	05-AUG-1999; 05-AUG-1999;	06-AUG-1999; 06-AUG-1999;	09-AUG-1999;	11-AUG-1999; 12-AUG-1999;	13-AUG-1999; 13-AUG-1999;	16-AUG-1999; 17-AUG-1999;	18-AUG-1999; 20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	23-AUG-1999; 23-AUG-1999;	25-AUG-1999; 26-AUG-1999;	27-AUG-1999;	27-AUG-1999; 30-AUG-1999;	31-AUG-1999; 01-SEP-1999;	07-SEP-1999;	13-SEP-1999;	16-SEP-1999;	20-SEP-1999; 22-SEP-1999;
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99US-0121825P. 99US-0123180P. 99US-0123548P. 99US-0125788P.	99US-0126264P. 99US-0126785P. 99US-0127462P. 99US-0128234P.	99US-0128714P. 99US-0129845P. 99US-0130077P.	99US-0130449P. 99US-0130510P.	99US-0130691F. 99US-0131449P. 99US-0132048P.	990S-0132407F. 990S-0132484F. 990S-0132485F.	99US-0132487F. 99US-0132487F. 99US-0132863F.	99US-0134218P. 99US-0134219P.	99US-0134221P. 99US-0134370P. 99US-0134768P.	99US-0134941P. 99US-0135124P.	99US-0135353P. 99US-0135629P.	99US-0136392P. 99US-0136392P. 99US-0136782P.	99US-0137222P. 99US-0137528P.	99US-0137724P.	99US-0138540P.	99US-0139119P.	99US-0139453P. 99US-0139492P.	99US-0139454P. 99US-0139455P.	99US-0139456P. 99US-0139457P.	99US-0139458P. 99US-0139459P.	99US-013946UF. 99US-0139461P.	99US-0139463P.	99US-013975UF.	99US-013981/F. 99US-0139899P.	99US-0140353P. 99US-0140354P.	99US-0140695P. 99US-0140823P.	99US-0140991P.	99US-0141842P.	99US-0142055P.
B-1999; R-1999; R-1999; R-1999;	R-1999; R-1999; R-1999; R-1999;	R-1999; R-1999; R-1999;	R-1999; R-1999;	X-1999; X-1999;	K-1999; K-1999; K-1999;	(-1999; (-1999; (-1999;	(-1999; (-1999;	(-1999; (-1999; (-1999;	(-1999; (-1999;	7-1999; 7-1999;	(-1999; (-1999; (-1999;	1-1999; 1-1999; 1-1999;	4-1999; 4-1999;	1-1999;	1-1999; 1-1999;	4-1999; 4-1999;	4-1999; 4-1999;	(-1999; (-1999;	1-1999; 1-1999;	1-1999;	1-1999;	1-1999;	1-1999;	1-1999; 1-1999;	1-1999;	N-1999;	1999;	1999;

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Enterococcus facetium encoding an Enterococcus facetium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 come of 10 fully defined sequences given in the (or comprising 40 composition in the comprising 40 complement or sequences hybridising to it). Also included are a crecombinant vector comprising the nucleic acid operably linked to creombinant vector comprising the nucleic acid operably linked to single-stranded probe comprising the nucleic acid operably linked to consortiption regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.

The nucleic acids is useful for disgnosing pathological conditions infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococus faccines in the present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                             The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%; Score 41; DB 7; Length 104; 66.7%; Pred. No. 23; ive 3; Mismatches 0; Indels
                                                                                                                    Example 1; SEQ ID NO 5890; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                 treating Enterococcus faccium infections. one if the disclosed E. faccium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA54377 standard; protein; 126 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein, SEQ ID 1945.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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           WPI; 2003-799836/75.
N-PSDB; ADC92609.
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FFFIPLINV
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104 AA;
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                                                                                           infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.7%; Score 42; DB 3; Length 221; 70.0%; Pred. No. 34; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC96263 standard; protein; 104 AA.
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           99US-0156596P.
99US-0157117P.
99US-0157853P.
99US-0158029P.
99US-0158232P.
99US-0158332P.
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9903-0159295P.
9903-0159330P.
9903-0159331P.
9903-0159637P.
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99US-0160741P.
99US-0160767P.
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99US-0160981P.
99US-0160989P.
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Matches 7; Conservative
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190 YFFLPVINXL 199
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07-OCT-1999;
08-OCT-1999;
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                            The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54011). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                     Claim 14; SEQ ID NO 1945; 205pp; English.
  WPI; 2003-395539/38.
N-PSDB; ADA52738.
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Gaps ö Query Match 66.1%; Score 41; DB 6; Length 126; Best Local Similarity 72.7%; Pred. No. 28; Matches 8; Conservative 1; Mismatches 2; Indels ઠે

Sequence 126 AA;

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Search completed: April 12, 2005, 08:18:19 Job time : 69.2 secs

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Sequence

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

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RESULT 2
US-09-107-532A-5890
is Sequence 5890, Application US/09107532A
is Patent No. 6583275
is Patent No. 6583275
is TITLE OF INVENTION:
is APPLICANT: Lynn A DOUCETC-Stamm and David Bush
intile OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
intile OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
is ENTRECOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
is CORRESPONDENCE ADDRESS:
is STREET: 100 Beaver Street
is STREET: Massachusetts
is COUNTRY: USA
                                                                                                                                                                                                                                                                                                                 Sequence 820, App
Sequence 1366, A
Sequence 16166, A
Sequence 126, App
Sequence 37747, A
Sequence 12, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 4493, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 4; Length 12; 100.0%; Pred. No. 0.00044; ive 0; Mismatches 0; Indels
         US-09-538-092-820

US-09-248-796A-23666

US-09-248-796A-3666

US-09-134-000C-3659

US-09-904-615-126

US-09-270-767-37747

US-09-077-675A-12

US-09-077-674-12

US-09-077-674-12

US-09-077-674-12

US-09-077-675A-10

US-09-077-675A-10
.09-949-016-11186
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US-09-077-675A-13
                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
2555
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US-09-641-803-4
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Sequence 5890, Ap
Sequence 35554, A
Sequence 6242, Ap
Sequence 7429, Ap
Sequence 7429, Ap
Sequence 456, App
Sequence 456, App
Sequence 12853, Ap
Sequence 12853, Ap
Sequence 12853, App
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Sequence 194, App
Sequence 4445, Ap
Sequence 11180, A
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Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 5836, Ap
Sequence 15770, A
Sequence 14873, A
Sequence 14925, A
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                                                                                     April 12, 2005, 07:49:30 ; Search time 14.0727 Seconds (without alignments) 63.654 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-107-532A-5890
US-09-270-76-35554
US-09-270-76-35554
US-09-270-76-35554
US-09-270-76-35564
US-09-26-291A-23368
US-09-205-258-456
US-09-107-532A-6843
US-09-107-532A-6843
US-09-489-039A-12853
US-09-489-035-194
US-09-134-000C-4445
US-09-489-033A-11180
US-09-489-033A-11180
US-09-489-033A-11180
US-09-489-033A-11180
US-09-311-021-138
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US-09-248-796A-14925
US-09-438-185A-999
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US-09-902-540-16439
US-07-649-591B-4
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US-09-902-540-15770
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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US-09-270-767-35554
US-09-270-767-35554
Sequence 35554, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Waleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35554
LENGTH: 235
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                                                                                                                                                                                                                                                                            ATORNAY/AGENT INPORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPAN: (781)893-507
INFORMATION FOR SEQ ID NO: 5890:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
                                                                             OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...104
SEQUENCE DESCRIPTION: SEQ ID NO: 5890:
                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 PAPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGHES SOURCE:
ORGANISM: Enterococus faecium
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 66.7
Matches 6; Conservative
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91 FFFIPLINV 99
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Matches 5; Conserv
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Sequence 6242, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
SOURCE OF SEQ ID NOS: 8252
LENGTH: 733
LENGTH: 733
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Sequence 50771, Application US/09270767

Sequence 50771, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: THO PAPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 50771

LENGTH: 235
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Best Local Similarity 41.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 6; Mismatches 1; Indels
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Pred. No. 37;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50771
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT CORGANISM: Acinetobacter baumannii US-09-328-352-6242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.5%;
50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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, OTHER INFORMATION: Xaa equals stop translation US-09-205-258-456
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EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER APPLICATION NUMBER: 60/048,998
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 456
LENGTH: 42
LENGTH: PRT
ORGANISM: Homo sapiens
                                                                                           EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
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APPLICATION WINBER: 60/048,916
APPLICATION DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
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EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
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                        048,894
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,893
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EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1997-06-06
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Patent No. 6610836

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7429
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                                                                                                                                                    Length 528;
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                                                                                                                                                    Score 39; DB 4;
Pred. No. 1.2e+02;
5; Mismatches 0
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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CURRENT PELLING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,890
EARLIER APPLICATION NUMBER: 60/048,996
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER PILING DATE: 1997-06-06
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EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 456, Application US/09205258 Patent No. 6525174 GENERAL INFORMATION:
                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7429
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                                                                                                                                                    62.9%;
50.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                 Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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130 YLFLPMINVL 139
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395 FFFMPILSIL 404
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; SEQ ID NO 23368
; LENGTH: 528
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APPLICATION NUMBER: 60/048,962
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Sequence 6843, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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Score 37; DB 4; Length 42;
Pred. No. 19;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIORITION DATE: US/09/107,532A
PRIOR APPLICATION NUMBER: US/09/107,532A
PRIOR APPLICATION DATE: 30-Jun-1998
APPLICATION NUMBER: 60/05,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 11,1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LOCATION: (B) LOCATION 1...72
SEQUENCE DESCRIPTION: SEQ ID NO: 6843:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-205-258-251
; Sequence 251, Application US/09205258
; Patent No. 6525174
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LENGTH: 72 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6843
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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 59.78;
75.08;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                              21 LPFFLPLI 28
                                                                            1 LFFFLPVV 8
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Best Local Similarity
Matches 6; Conserv
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US-09-107-532A-6843
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PPLICANT: Young et al. (TILE OF INVENTION: 207 Human Secreted Proteins
                                                                                                 NT FILING DATE: 1998-12-04

ER APPLICATION NUMBER: PCT/US98/11422

ER FILING DATE: 1999-06-04

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/049, 375

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048, 881

ER FILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06
                                                                             CURRENT APPLICATION NUMBER: US/09/205,258
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
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FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,883
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/046
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EARLIER APPLICATION NUMBER: 60/046
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APPLICATION NUMBER: 60/
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Sequence 194, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
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Pred. No. 32;
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                                                                                   ZIP: 20850
ZIP: 20850
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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---CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                       Maryland
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PVVNVLP 12
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                      CITY: Rockville
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                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                    COUNTRY:
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APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NEWONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT PAPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12853
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APPLICANT: Gil H. Choi
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 4; Length 405;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE

LOCATION: (103)

; OTHER INFORMATION: Xaa equals stop translation

US-09-205-258-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
              EARLIER APPLICATION UNBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATCHTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-489-039A-12853
; Sequence 12853, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-071.035-196
'Sequence 196, Application US/09071035
'Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.7
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.7
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 FFRPAVNFLP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 FFLPVVNVLP 12
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 LFFFLPLI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LFFFLPVV 8
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 251
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Gaps

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APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PEPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11180
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-134-000C-4445
; Sequence 4445, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
    APPLICANTION:
    APPLICANTION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.1%; Gcore 36; DB 4; Length 137; 45.5%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%; Scc...
100.0%; Pred. No. ...
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; Sequence 11180, Application US/09489039A
; Patent No. 6610836
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE GHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-09-071-035-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PVVNVLP 68
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Best Local Similarity
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Sequence:

Searched:

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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

AND

TITLE OF INVENTION:

ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

FILE REFERENCE: 265.0022010

TITLE OF INVENTION:

WINER:

GURENY APPLICATION NUMBER:

GOOD-028

FRIOR FILING DATE:

CURRENY APPLICATION NUMBER:

FRIOR FILING DATE:

BRIOR FILING DATE:

BRIOR APPLICATION NUMBER:

GOOD-08-17

FRIOR FILING DATE:

SOFTWARER

SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 62; DB 14; Length 12; 100.0%; Pred. No. 0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: peptide
US-10-281-652-4
US-10-424-599-252118

US-10-094-749-1945

US-10-094-749-1945

US-10-424-599-171577

US-10-424-599-171577

US-10-427-963-138531

US-10-425-114-42601

US-10-425-114-42601

US-10-424-599-184927

US-10-424-599-1849052

US-10-424-599-1849052

US-10-424-599-184046

US-10-424-599-208134

US-10-424-599-208134

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-208168

US-10-424-599-2888

US-10-424-599-2888

US-10-427-963-1107198

US-10-427-963-1107198

US-10-427-963-1107198

US-10-427-963-1107198

US-10-424-599-235499

US-10-424-599-235499

US-10-424-599-235499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-764-877-1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LFFFLPVVNVLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 211893,
Sequence 143141,
Sequence 227817,
Sequence 260138,
Sequence 260138,
Sequence 245079,
Sequence 245079,
Sequence 2599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Appl
Sequence 261912,
                                                                                                                                                            April 12, 2005, 07:49:30 ; Search time 37.2 Seconds (without alignments) 107.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_RW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7/cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                          GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-281-652-4
US-10-691-330-4
US-10-424-599-261912
US-10-424-599-211893
US-10-424-599-218141
US-10-424-599-218474
US-10-424-599-226138
US-10-424-599-245079
US-10-424-599-245079
US-10-424-599-245079
US-10-424-599-245079
US-10-424-599-184599
US-10-424-599-184599
US-10-424-599-184599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1418010 seqs, 331997259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                            1 LFFFLPVVNVLP 12
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Match Length DB
                                                                                                                                                                                                                                                           US-10-691-330-4
62
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12
96
47
47
190
197
678
678
678
548
101
101
81
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100.0
72.6
71.0
69.4
69.4
69.4
67.7
67.7
67.7
66.1
66.1
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00044666661111
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Gaps

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Indels

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Result

Sequence 49461, A
Sequence 204168, Sequence 144849, Sequence 192194, Sequence 192194, Sequence 456, App Sequence 456, App Sequence 196117, Sequence 235499, Sequence 235499, Sequence 24750, A Sequence 1107, App Sequence 110

181046, 237727, 164024, 167720,

Sequence 2 Sequence 1 Sequence 1

Sequence 1 Sequence 1 Sequence 2 Sequence 1

Sequence 1 Sequence 2 Sequence 1 Sequence 3 Sequence 4

```
**APPLICANT: La Rosa Thomas J

**APPLICANT: Cavalic David K

**APPLICANT: Cao Yongwei

**TITE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With

**TITE OF INVENTION: Plants and Uses Thereof for Plant Improvement

**FILE REFERENCE: 38-21(5323)8

**CURRENT PAPLICATION UNBER: US/10/424,599

**CURRENT FILING DATE: 2003-04-28

**NUMBER OF SEQ ID NOS: 285684

**SEQ ID NO 211893

**LEMBER OF SEQ ID NOS: 285684

**LEMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 143141, Application US/10424599
Sequence 143141, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomás J
APPLICANT: Kovalic David K
APPLICANT: Zou Yihua
APPLICANT: Zou Yihua
APPLICANT: Zou Yihua
APPLICANT: Zou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 143141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LA ROSA Thomas J
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: PAT_MRT3847_33366C.1.pep
US-10-424-599-211893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_10026C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 227817, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
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Matches 7; Conservative
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FFILPITNALP
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
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Fublication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERRENCE: 39-21 (3523.9)
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 261912
                                                                                                                                                                                                                                                                            APPLICANT: Station, G. John
APPLICANT: Station, G. John
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Kruzel, Marian
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
FILE REPERENCE: 265.00390101
CURRENT APPLICATION NUMBER: US/10/691,330
CURRENT FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PARENTIN VERSION 3.2
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 15; Length 96;
Pred. No. 4.9;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_78529C.1.pep
US-10-424-599-261912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Synthetic Peptides US-10-691-330-4
                                                                                                                                                                                    ; Sequence 4, Application US/10691330; Publication No. US20050042300A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.6%;
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                                                                                                                                                                                                                                                             APPLICANT: Boldogh, Istvan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LFFFLPVVNVLP 12
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12 FFFFWVSVFP 22
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ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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US-10-424-599-211893 ; Sequence 211893, Application US/10424599 ; Publication No. US20040031072A1

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Gaps ;

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Vinus A
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5)223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 245079
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREEMENT: 32-163233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBOO ID NO 197974
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                                                                                                                                                                                                                                                                                                             Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_20796C.1.pep
US-10-424-599-197974
                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_76929C.1.pep
US-10-424-599-260138
                                                                                                                                                                                                                                                                                                         Query Match 69.4%; Score 43; DB 15; Best Local Similarity 77.8%; Pred. No. 80; Matches 7; Conservative 2; Mismatches 0
                            FEATURE:
NAME/KEY: unsure
LOCATION: (1).. (678)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 63.6
Matches 7; Conservative
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74 LFFYLPVIN 82
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ORGANISM: Glycine max
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ORGANISM: Glycine max
ORGANISM: Glycine max
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| Publication No. US20040031072A1 |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: AND YINUA |
| APPLICANT: Cao Yongwei |
| TITLE OF INVENTION |
| TITLE OF INVENTION
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Publication No. US20040031072A1
GENERAL INCOMMATION:
BAPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER: OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 15; Length 180;
Pred. No. 20;
2; Mismatches 0; Indels
                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_47747C.1.pep
US-10-424-599-227817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_3930C.1.pep
US-10-424-599-218474
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LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 227817 LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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125 LFFYLPVIN 133
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ORGANISM: Glycine max
                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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LENGTH: 678
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Sequence 228846, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424, 599
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 228846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 252118, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Can Vorsic David K
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_48675C.1.pep
US-10-424-599-228846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_69690C.1.pep
US-10-424-599-252118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.1%; Score 41; DB 15;
60.0%; Pred. No. 19;
iive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1
Pred. No. 19;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: SOGAI, TAKAO
APPLICANT: GUGIYANA, TOWOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LFFFLPV--VNVLP 12
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Glycine max
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11 FLVPIVNILP
                                       JS-10-424-599-228846
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US-10-424-599-252118
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Sequence 154599, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (3523.9)

CURRENT APPLICANT: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

SEQ ID NO 154599
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234012
LENGTH: 54
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   Score 42; DB 15; Length 101;
Pred. No. 16;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.1%; Score 41; DB 15; Length 54; 100.0%; Pred. No. 13; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 41; DB 15; Length 56; 63.6%; Pred. No. 13; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_110624C.1.pep
US-10-424-599-154599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53337C.1.pep
US-10-424-599-234012
                                                                                                                                                                                                                                                                                                                                              Sequence 234012, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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76 FFFLPIVN 83
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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US-10-424-599-154599
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18 LFFFLPISTIL 28

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SATO, HIROYUKI

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66.1%; Score 41; DB 15; Length 126; 72.7%; Pred. No. 30; tive 1; Mismatches 2; Indels
APPLICANT: ISONO, YUUKU
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
APPLICANT: NAGAI, KEJICHI
APPLICANT: NAGAI, KEJICHI
APPLICANT: IRLE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: WASHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TILE OF INVENTION: NOWEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: 0750-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALENT VET.
SOFTWARE: PALENT VET.
SEQ ID NO 1945
TYPE: PRT
CORRANISM: Homo sapiens
US-10-094-749-1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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2 FFFLPVVNVLP 12

Gaps ö

Search completed: April 12, 2005, 07:55:21 Job time : 38.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

April 12, 2005, 07:49:31; Search time 8.61818 Seconds (without alignments) 133.973 Million cell updates/sec

US-10-691-330-4 62 1 LFFFLPVVNVLP 12 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ption	enterobactin synth				NADH2 dehydrogena	probable membrane	spa29 protein - Sh	hypothetical prote	hypothetical prote	lipopolysaccharide	drug efflux transp	quinate transport	cyclic nucleotide	hypothetical prote	heme exporter prot	SN-glycerol-3-phos	hypothetical prote	probable amino aci	probable amino aci	ami	w	hypothetical prote	_	probable cyclic nu	hypothetical prote	secretory protein	spaR protein - Sal	probable apolipopr	
, <b>B</b>	AB3519	D90125	AI2652	S49114	D70420	S61200	149846	T21247	S74688	F72257	E83002	G31277	T52573	AD2302	AF3483	D98345	AC2937	H85755	C64878	A90863	G82872	G84682	E86294	H86330	T15420	AD0851	837309	G71348	0000
DB	~	~	~	~	~	~	~	~	~	~	~	7	~	7	7	N	~	7	7	7	7	7	~	~	~	7	~	0	•
Length	469	144	62	99	488	692	256	359	391	471	509	537	710	364	221	296	296	461	479	479	532	678	738	746	218	263	9	546	
& Query Match	77.4	72.6	71.0	66.1	66.1	66.1	65.9	65.9	65.9	62.9	62.9	62.9	62.9	62.1	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	t
Score	48	45	44	41	41	41	39	39	39		39	39	39	38.5	38	38	38	38	38	38	38	38	38	38	37	37	37	37	
Result No.	-	7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	6

hypothetical prote hypothetical prote and fare/thican far	polysacharide ABC phospho-N-acetylmu carboxypeptidase B	hypothetical prote conserved hypothet	carboxypeptidase B probable vibriobac hyporhetical prote	cytochrome P450 mo hypothetical prote	uridine kinase-rel hypothetical prote
S76608 T33593	A69286 E72402 CPBOB	AB0979 F90011	A32129 H82280 T30602	T52170 T02898	B72341 D85013
000	4 6 6 6	00-	1000	0 0	0 0
118 201	3022	310	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	501 505	555 689
58.1	58.1 1.88.1 1.00.1	58.1	58.1	58.1	58.1 58.1
999	9 9 9 9 9 9 9 9	36	9 9 9 9	900	36 36
30	7 M M M M	376	0 6 4 4 0 0 0 L	. 4. 4. 4.0 &	44 45

## ALIGNMENTS

enterobactin synthetase component F [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

CjAccession: AB3519 (G.) Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688 A;Recession: AB3519 A;Recession: AB3519 A;Recession: AB3519 A;Recession: Lype: DNA A;Residues: 1-469 < KUR>

A;Cross-references: UNIPROT: Q8xDU8; GB: AE008918; PIDN: AAL53317.1; PID: g17984203; GSPDB: GA;Experimental source: strain 16M

C;Genetics: A;Gene: BMEII0076 A;Map position: II

Gaps ö Length 469; 1; Indels Score 48; DB 2; Pred. No. 1; 2; Mismatches Query Match

Best Local Similarity 72.7%;
Matches 8; Conservative 2

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374 FFESPLINVLP 384 2 FFFLPVVNVLP 12 q ઠ

hypothetical protein orf144 [imported] - Guillardia theta nucleomorph C; Species: nucleomorph Guillardia theta
C; Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: D90125
R; Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei Mature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671, PMID:11323671

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-114 <-DOUS-A;Cross-references: UNIPROT:Q98S86; GB:AF083031; NID:g13794319; PIDN:AAK39696.1; GSPDB:G

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A; Map position: 3 A; Genome: nucleomorph C; Keywords: nucleomorph

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C;Species: Aquifex aeolicus
C;Date: Ob-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accesion: D70420
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-488 <AQF>
A;Cross-references: UNIPROT:067391; GB:AE000737; NID:g2983782; PIDN:AAC07354.1; PID:g298C
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiSasakawa, C.; Komatsu, K.; Tobe, T.; Suzuki, T.; Yoshikawa, M.
J. Bacteriol. 175, 2334-2346, 1993
A/Title: Eight genes in region 5 that form an operon are essential for invasion of epithe A;Reference number: A49846; MUID:93224456; PMID:8385666
A;Retens: I49846
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: Q06665; EMBL: U28374; NID: 9849207; PIDN: AAB64750.1; PID: 984926
                                                                                                                                                                                             Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70420
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: hypothetical protein D9740.21
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S61200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spa29 protein - Shigella flexneri plasmid pMYSH6000
C;Species: Shigella flexneri
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: I49846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: nuoN2
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R,Ding, H. submitted to the EMBL Data Library, June 1995
A,Description: The sequence of S. cerevisiae cosmid 9740.
A,Reference number: S61160
A,Accession: S61200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gross-references: SGD:S0002722
A;Cross-references: SGD:S0002722
A;Map position: 4R
C;Superfamily: yeast probable membrane protein YDR314c
C;Keywords: transmembrane protein
P;94-110/Domain: transmembrane #status predicted <TM1>F;239-255/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane protein YDR314c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%;
58.3%;
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242 LPFFIILENVLP 253
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUD:21608550; PMID:11743193

A;Refatus: preliminary

A;Status: preliminary

A;Residues: DNA

A;Residues: 1-62 «KUR»

A;Cross-references: UNIPROT:Q8UHQ7; GB:AE008688; PIDN:AAL41639.1; PID:g17738979; GSPDB:G

C;Genetics: A;Cross-references: A;Gene: Atuo623

A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: A12652
R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Atu0623 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849114
hypothetical protein - yeast (Williopsis suaveolens) mitochondrion (fragment)
C;Species: mitochondrion Williopsis suaveolens
C;Date: 16-Peb-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 849114
R;Nosek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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               Length 144
                                                                                    Indels
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                                                                                    5
               DB 2;
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Pred. No. 0.69;
2; Mismatches
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Pred. No. 2.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subjects to the EMBL Data Library, January 1994
A, Reference number: 849114
A, Accession: 849114
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-66 < NOS>
                                                                             2; Mismatches
       Score 45;
Pred. No.
       72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative ;
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50.0%;
Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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24 IFFFLKKVNILP 35
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Best Local Similarity 50.0
Matches 6; Conservative
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LFFFIMIIGVMP 48
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FYSLPVMNVLP 15
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A)Genetic code: SGC2
C)Keywords: mitochondrion
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lipopolysaccharide biosynthesis protein-related protein - Thermotoga maritima (strain MSE
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399, 323-329, 1999
Aftile: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:09X1C5; GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD3647:
A;Experimental source: strain MSB8
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RjStover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br addan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A.jtile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoral A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CjAccession: 804254; G31277 — Tyler, B.M.; Patel, V.B.; Rutledge, B.J.; Case, M. Rigeever, R.F.; Huiet, L.; Baum, J.A.; Tyler, B.M.; Patel, V.B.; Rutledge, B.J.; Case, M. J. Holl. Biol. 207, 15-34, 1989
A,Title: DNA sequence, organization and regulation of the qa gene cluster of Neurospora
                                                                                                                                                                                                                                                                            C;Accession: F72257
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:085163; GB:AE004928; GB:AE004091; NID:g9951450; PIDN:AAG0854
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug efflux transporter PA5160 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GJ1277; Transport protein - Neurospora crassa (tentative sequence)
quinate transporter
C;Species: Neurospora crassa
C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 471;
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Pred. No. 41;
5; Mismatches
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Best Local Similarity
Loc 8; Conserve
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G31277
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A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-391 «KAN>
A;Cross-references: UNIPROT:P72824; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1683
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A,Molecule type: DNA
A,Residues: 1-256 <SAS>
A,Residues: 1-256 <SAS>
A,Residues: 1-256 <SAS>
A,Grosdues: 1-256 <SAS>
C,Genetics: Dlasmily: Diplomation of the control of th
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Auriety: PCC 6803
C;Accession: S74688
S;Xanko, T.; Saco, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:017830; EMBL:283106; PIDN:CAB05493.1; GSPDB:GN00023; CESP:FZ
A;Experimental source: clone F22B8
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R;McMurray, A.
R;McMurray, A.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19396
A;Reference number: Z19396
A;Reference pumber: Z19396
A;Reference pumber: Z19396
A;Reference number: Z19396
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                                                                                                                                                                                                                                                                                                                   Query Match 62.9%; Score 39; DB 2; Length 256; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.9%; Score 39; DB
larity 70.0%; Pred. No. 29;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 5
A;Introns: 96/3; 132/2; 161/3; 200/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 LVFFLPIANV 108
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LFFFLPFLN 35
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Matches 7; Conserv
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A;Gene: CESP:F22B8.1
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Indels

DB 2; Length 364;

Reference number: S04250; MUID:89293848; PMID:2525625

us-10-691-330-4.rpr

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A,Cross-references: UNIPROT:Q8YQ64; GB:BA000019; PIDN:BAB75670.1; PID:g17133105; GSPDB:GA A,Experimental source: strain PCC 7120
C;Genetics:
A,Gene: a113971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesscrence. Matl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688
A;Accession: AF3483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8YEM6; GB:AE008917; PIDN:AAL53033.1; PID:g17983891; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heme exporter protein B [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                     Score 38.5; I
Pred. No. 36;
                                                                                                                                                                                                                                                                    2; Mismatches
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281 LFFFAALISINLAVINILP 299
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                                                                                                                                                                                           Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
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   1-364 <KUR>
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A;Molecule type: DNA
A;Residues: 1-221 <KUR>
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A, Residues:
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T52573
Cyclic nucleotide and calmodulin-regulated ion channel [imported] - Arabidopsis thaliana cyclic nucleotide and calmodulin-regulated ion channel [imported] - Arabidopsis thaliana (species: Atabidopsis thaliana (mouse-ear cress)
C; Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C; Accession: T5573
R; Kohler, C.; Merkle, T.; Neuhaus, G.
Plant J. 18, 97-104, 1999
A; Reference number: Z26120
A; Reference number: Z26120
A; Reference number: Z2573
A; Reference number: Manay; translated from GB/EMBL/DDBJ
                                                                               ross-references: UNIPROT:P11636; EMBL:X14603; NID:93060; PIDN:CAA32752.1; PID:93065
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                                                                                                                                                                                                                                                                                                             F)99-119/Domain: transmembrane #status predicted cTM03-
F;132-152/Domain: transmembrane #status predicted cTM04-
F;161-181/Domain: transmembrane #status predicted cTM05-
F;286-306/Domain: transmembrane #status predicted cTM06-
F;286-306/Domain: transmembrane #status predicted cTM06-
F;36-376/Domain: transmembrane #status predicted cTM09-
F;350-410/Domain: transmembrane #status predicted cTM109-
F;427-447/Domain: transmembrane #status predicted cTM10-
F;459-479/Domain: transmembrane #status predicted cTM10-
F;459-479/Domain: transmembrane #status predicted cTM10-
F;459-479/Domain: transmembrane #status predicted cTM12-
                                                                                                                                                                                Superfamily: maltose transport protein MAL61

Seywords: transmembrane protein

2-42/Domain: transmembrane #status predicted <TM01>

67-87/Domain: transmembrane #status predicted <TM02>
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475 IYFFLPVTKSIP 486
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nes 6; Conservative
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                                             -537 <GE2>
                        Molecule type: DNA
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                                          Score 38; DB 2; Length 221;
Pred. No. 27;
4; Mismatches 2; Indels
A;Map position: I
C;Superfamily: cytochrome c biogenesis protein CycW
                                                                                                                                                                                      Search completed: April 12, 2005, 07:56:51
Job time : 10.6182 secs
                                              61.3%;
50.0%;
                                                           Local Similarity 50.0
                                                                                                           1 LFFFLPVVNVLP 12
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23 ILFFLAVISVMP 34
                                               Query Match
                                                              Best Loca
Matches
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakases. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Status: preliminary

AD2302
hypothetical protein all3971 [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession: AD2302

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Gaps

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62.9%; Score 39; DB 2; Length 710; 75.0%; Pred. No. 57;

2; Mismatches

Conservative

Query Match Best Local Similarity

110 FFYLPVIN 117

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2 FFFLPVVN 9

A; Kresidues: 1-710 «KOH»
A; Cross-references: UNIPROT: QRRWS9; EMBL: Y17913; PIDN: CAB40130.1
A; Experimental source: cultivar Columbia
A; Genetics:

A, Gene: BMEI1852

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Query Match
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Q8FXP8;
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Q8FXP8
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Q99873
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Q86683
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Q89811
Q73qu3
Q9xwu8
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Q6zg24
Q7x641
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Q6jt28
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                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q98S86
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O24102
Q8FUV9
Q8VQL7
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Q652Z3
Q652Z3
Q052Z3
Q06665
Q06665
Q783H1
Q6K9X2
Q8PUB3
Q73QU3
Q73QU3
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Gapop 10.0 , Gapext 0.5
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Q7M9X9
Q36231
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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STRAIN-16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
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                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brucella suis.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 469 AA; 53074 MW; 17A7B73A02428D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Enterobactin syntherase, component F, putative.
OrderedLocusNames=BRA0017;
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
EMBL; AE009646; AAL53317.1; -.
PIR; AB3519; AB3519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%; Score 48; DB 2;
llarity 72.7%; Pred. No. 6.8;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 AA.
      469 AA
                                                         01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last seq 01-UTN-2003 (TrEMBLrel. 24, Last and ENTEROBACTIN SYNTHETASE COMPONENT F.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q9KTV9; 1L5A.
Pfam; PF00668; Condensation; 1.
                                                                                                                                                                           OrderedLocusNames=BMEII0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 FFFSPLINVLP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FFFLPVVNVLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                               STRAIN-Dupont;
MEDLINE-ZIG08550; PubMed=11743193; DOI=10.1126/science.1066804;
MEDLINE-ZIG08550; PubMed=11743193; DOI=10.1126/science.1066804;
Wood D.W., Setubal J. C., Kaul R., Mond G.E., Almeida N.F. Jr., Woo L.,
Chan Y., Raulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Lim -J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung W. Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                      Agrobacterium tumefaciens (strain C58 / ATCC 33970). asteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobiaceae; Agrobacterium group; Agrobacterium. VCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 71.0%; Score 44; DB 2; Length 218; Local Similarity 54.5%; Pred. No. 16; es 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 50310;

Burger G., O'Kelly C.J., Gray W.M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF295846; AAG13700.1;
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AA; 25870 MW; EF7A162FEF8BD674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE009030; AAL41639.1; -.
PIR, AI2652; AI2652.
Complete proteome; Hypothetical protein.
SEQUENCE 62 AA; 7135 MW; C67C9F18234FEAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
U-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
ABC transporter channel subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 5.1;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AA
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Eukaryota; Malawimonadidae; Malawimonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O24102;
01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:2317-2323(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malawimonas jakobiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LFFFLPIITII 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FFFLPWWVLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYSLPVMNVLP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LFFFLPWNWL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=136089;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=yejV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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Q9G873
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셤
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             SEQUENCE FROM N.A.
STRAIN=130 / Bicvar 1,
MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L.A., Brinker L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
Eighterg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
MEDILINE=2123349; PubMed=11123671; DOI=10.1038/35074092;
MEDINE=2123349; PubMed=11123671; DOI=10.1038/35074092;
DOUGHAS S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T., Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001); AAK39696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                      "The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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Pred. No. 6.8;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.6%; Score 45; DB 2; Length 144; 66.7%; Pred. No. 7.5; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL) ALCONOCCE, D90125.
PJR, D90125.
Hypothetical protein; Nucleomorph.
Hypothetical protein; Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 AA; 52986 MW; AD46038DCF854A31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                            animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
EMEL, AE014506; AAN33229.1;
HSSP; OSKTV9; 1L5A.
TIGR; BRA0017; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98S86;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
Hypothetical protein orf144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guillardia theta (Cryptomonas phi).
Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001242; Condensatn.
Pfam; PF00668; Condensation; 1.
Complete proteome.
SEQUENCE 469 AA; 52986 MW: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.4%;
Best Local Similarity 72.7%;
Matches 8; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 FFFSPLINVLP 384
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Q8UHQ7;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          098886
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1098886
10 09888
AC 0988
DT 01-0
DT 01-0
DT 01-0
DE HYPO
GN Nucl
OC Nucl
OC Nucl
OC Nucl
CR Nucl
RA MEDL
RA DOUG
RA DOUG
RA MU X
RA MEDL
RA MU X
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RA MU X
RA MU X
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RA MU X
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Q8UHQ7
ID Q8UH
AC Q8UH
DT 01-J
DT 01-J
DE HYPO
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Gaps

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Gaps

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SO DE REPRESENTATION OF STANK REPRESENTATION OF STANK

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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales;
Thermoplasmataceae, Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 288;
                                                                                                                                                                                      Length 271;
                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               Complete proteome, Transmembrane, Transport. SEQUENCE 271 AA, 29759 MW, 6DDEC475BD4C1A83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Transport.
SEOUENCE 288 AA; 31696 MW; B5C20EA208DCFD8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat.
Putative ABC transporter permease protein B.
Name=BaTn1953.ORF9;
                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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Pred. No. 21;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   288 AA
                                                                                                                                                                                                                            2; Mismatches
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                                                                          InterPro; IPR000515; BPD_transp
                                                                                          Pfam; PF00528; BPD transp 1; 1. PROSITE; PS50928; ABC TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00528; BPD_transp_1; 1.
PROSITE; PS50928; ABC_TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytochrome b related protein. OrderedLocusNames=Tal228;
                                                                                                                                                                                      71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.0%;
                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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31 LFFFYPLVNLL 41
                                                                                                                                                                                                                                                                 1 LFFFLPVVNVL 11
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14 LFFFYPLVNLL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=235;
   TIGE; BRA1106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bricker B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   Q8VQL7
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Q8VQL7
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   OCCUPATION
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Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

-!- FUNCION: Part of a binding-protein-dependent transport system.

Probably responsible for the translocation of the substrate across the membrane (By similarity).

-!- SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the binding-protein-dependent transport EMBL; AE014602; AAN34268.1; -.
                                                                                                                                                                                                                                           Gamas P., de Carvalho Niebel F., Lescure N., Cullimore J.;
"Use of a subtractive hybridization approach to identify new Medicago
truncatula genes induced during root nodule development.";
Mol. Plant Microbe Interact. 9:233-242(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-1330 / Biovar 1;
MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
Paulben IT. Seahadari R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.NCBI_TaxID=3880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.0%; Score 44; DB 2; Length 249; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                 Gamas P.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
Polyamine ABC transporter, permease protein, putative.
GrideredLocusNames=BRA1106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA; 26923 MW; 4BF9256A0FDD1318 CRC64;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA
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                                                                          Medicago truncatula (Barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003612; AAI.
Pfam; PP00234; Tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                          MEDLINE=96212994; PubMed=8634476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y15372; CAA75594.1;
HSSP; P24337; 1HYP.
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                                         MtN4 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Root nodule;
                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Root nodule;
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hes 8; Conserv
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RESULT 7
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Gaps . 0

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SEQUENCE

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RESULT 10 Q8A411

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MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
A MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
A Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
A Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
A Moyer F., Lederer H., Schuster S.C.;
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Complete genome sequence and analysis of Wolinella succinogenes.";
T. Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003)
T. -- SIMILARITY: Belongs to the sodium:solute symporter (SSF) family.
R. EMBL; BRS71658; CAE09732.1; --
R. GO; GO:0016021; C:inteapral to membrane; IEA.
R. GO; GO:0016215; F:transporter activity; IEA.
R. GO; GO:0005215; F:transporter activity; IEA.
R. InterPror. IPRO.1734; Na/Solut_symport.
                       Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Wolinella.
NCBL_TaxID=844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Williopsis.
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Pred. No. 18;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X77238; CAA54455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00457; NA_SOLUT_SYMP_2; UNKNOWN_1.
PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
Complete proteome; Transmembrane; Transport.
SEQUENCE S85 AA; 63119 WW; 362293F8529FA91D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
66 AA; 7586 MW; 78C9BCF9A31B94FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Partial putative ORF (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S49114; S49114.
GO; GO:0005739; C:mitochondrion; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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50.0%;
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01-NOV-1996 (TrEMBLrel. 01,
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Best Local Similarity 63.0
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523 FFFIPGTNLLP 533
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37 LFFFIMIIGVMP 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00474; SSF; 1.
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                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=58637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CBS 255;
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SEQUENCE
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Q96NK3;
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Q96NK3
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MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Blursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
ENBL, AE016937; AA077899.1; -.
InterPro; IPR000412; ABC 2.
InterPro; IPR000890; ABC2_MEMBRANE; UNKNOWN_1.
SCOMPLE Proceome.
SEQUENCE 545 AA; 61484 MW; 976E2EF859984466 CRC64;
                                                                                STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%; Score 44; DB 2; Length 525; 75.0%; Pred. No. 37; trive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2; Length 545;
Pred. No. 85;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 AA; 58544 MW; 145564FA78C665B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Putative MFS transporter.
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                             Nature 407:508-513(2000).

EMBL, AL445066; CAC12352.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:006118; P:electron transport; IEA.

InterPro; IPR005797; Cytb b6 N.

Pfam; PF00033; Cytochrom BN; 1.

Complete protecome.
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01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity 70.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| ||:| |||
368 LFFILPLVIVLP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=BT2793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SODIUM/SOLUTE SYMPORTER,
OrderedLocusNames=WS0601;
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24 LFFFLPILSV 33
                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=2303;
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Gaps

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Q7M9X9;

Separate

QXMMY9

RESULT 11 Q7M9X9

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clone:0SJNBa0043B22.";
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SEQUENCE 1
                                                                                            Query Match
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                                                                                                                                                                             RC TISSUE=Brain;

PUDMed=14702039; DOI=10.1038/ng1285;

RA OFA T., SULUKI Y., NISHIKAWA T., ORGUKI T., SUGIYAMA T., ITTE R.,

RA OFA T., SULUKI Y., NISHIKAWA T., ORGUKI T., SUGIYAMA T., ITTE R.,

RA OFA T., SULUKI Y., NISHIKAWA T., ORGUKI T., TANAKITA H.,

RA SEKINE M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA MARAMASHI K., Yasuda T., IWAYANASI T., Wagateuma M., Shiratori A.,

RA MARAMASHI M., Kanda K., Yokoi T., Furnya T., Kikkawa B., Omura Y.,

RA DE K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Anai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Narehorii K., Takibashi-Fujii A., Hara H., Tanase T., Nomura Y.,

RA Kanehorii K., Takhashi-Fujii A., Hara H., Tanase T., Nomura Y.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Imose N.,

Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Noshikawa Y., Matunawa H., Ichihara T., Shiohata N., Sano S.,

Nomiyama H., Satoh N., Takami S., Fukuzumi Y., Rawakami B.,

RA Masagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Masagawa S., Senoh A., Mizoguchi H., Tanas S., Fukuzumi Y.,

RA Masagawa S., Senoh A., Mizoguchi H., Tanas S., Fukuzumi Y.,

RA Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Namazaki M., Watanabe Y., Noguchi S., Itoh T., Shigeta K., Senba T.,

Rabimura K., Pakakami T., Oyama M., Hata H., Watanabe M., Komatsu T.,

Matsumura K., Nakajima Y., Mituno T., Morinaga M., Sasaki M.,

Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

Matsumura K., Nakajima Y., Mituno T., Morinaga M., Sasaki M.,

Rabasaki K., Yada T., Nakamura V., Ohara O., Isogai T., Sukagano S.,

Nokumura K., Nakajima Y., Ohara O., Isogai T., Sukagano S.,

Ra Rabasa M., R
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cyclic nucleoride-gated calmodulin-binding ion channel-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 126;
Pred. No. 33;
1; Mismatches 2; Indels
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EMBL; AK055252; BAB70890.1; -.
SEQUENCE 126 AA; 14391 MW; D1B23CDB0644847B CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FL730690.
Homo sapiens (Human).
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ilarity 72.7%;
Conservative
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Best Local Similarity
19, Conserve
                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the human malaria parasite Plasmodium
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AP005470; BAD46124.1; -. SEQUENCE 242 AA; 27613 MW; 168B4C5E7991E868 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Naturė 419:498-511(2002).
EMBL; AE014816; AAN36634.1; -.
SEQUENCE 376 AA; 45051 MW; 0FDE636678149F2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Exopolyphosphatase, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                             Score 41; DB 2
Pred. No. 60;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             376 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 12, 2005, 08:05:42 Job time : 59.9454 secs
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                   66.1%;
                                                                                                                                                    6; Conservative
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74 LFFYIPVIN 82
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les 6; Conserv
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                                                                                                                             Local Similarity
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us-10-691-330-5.rag

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein April 12, 2005, 07:49:31 ; Search time 84 Seconds (without alignments) 69.064 Million cell updates/sec Run on:

US-10-691-330-5 Title: Perfect score:

1 DLEMPVLPVEPFFV 15 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp1980s:*
geneseqp2000s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001ss:*
geneseqp2003bs:*
geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Add33586 Acinetoba Add08702 Ciona int	Adio0525 Aspergiii Abg06766 Novel hum Ado29919 Human sec	Abp79310 N. gonorr Abb60555 Drosophil	Abo79615 Pseudomon Ads29748 Bacterial			Abo53682 Novel hum		Abg10974 Novel hum		Aag48755 Arabidops		Aag48761 Arabidops
ADA33586 ADQ08702	ADP29919	ABP79310 ABB60555	ABO79615 ADS29748	ABB61392	AAGU1/34 AAY86518	ABO53682	ABG14725	ABG10974	ABB11472	AAG48755	ABB71049	AAG48761
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44	4 . 4 . 4 2 . 5 5	44	4 4 2 2	42	41.5	41.5	41.3	41	41	41	41	41
27	7 7 8 7 8 8	31	33	35	37	38	ນ 4. ນຸດ	41	42	43	44	45

## ALIGNMENTS

Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient Dermatological; oxidative stress regulator; colostrinin. Boldogh I; Ä. Claim 6; Page 25; 48pp; English. AAB72504 standard; peptide; 15 17-AUG-2000; 2000WO-US022665. 99US-0149310P. (first entry) (TEXA ) UNIV TEXAS SYSTEM. Stanton GJ, Hughes TK, Colostrinin peptide #5. WPI; 2001-218342/22. WO200112650-A2. Unidentified. 17-AUG-1999; 09-MAY-2001 22-FEB-2001. AAB72504; RESULT 1 AAB72504 

Sequence 15 AA;

Gaрв ö Length 15 Indels Query Match 100.0%; Score 81; DB 4; L Best Local Similarity 100.0%; Pred. No. 1.4e-05; Matches 15; Conservative 0; Mismatches 0;

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à 셤 AAB59322;

RESULT 2 AAB59322 Ovis sp.

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a proline rich polypeptide aggregate confained in colostrum. The peptides have immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing inducing blood cell proliferation. The peptides are useful for inducing thouse and for interaction. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders, mental disorders, dementia, neurodegenerative diseases, ablabiance's diseases, motor neurone disease, psychosis, neurosis, disorders of the immune system, bacterial and viral infections and acquired immunological deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
   dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuroprotective; neural cell differentiation regulator; colostrinin;
                                                                                                                                                                                                                                                                                                                                                              Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
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Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 34; 50pp; English.
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REGEN THERAPEUTICS PLC.
                                                                                                                                                                  17-AUG-2000; 2000WO-US022818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                   99US-0149311P.
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Les 15; Conservative
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                                                                                                                                                                                                                                                                                            Hughes TK,
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                        infection
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                                                                                            WO200111937-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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                                                                                                                                                                                                  17-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2001
                                                                                                                                                                                                                                                                                            Stanton GJ,
                                                                                                                                22-FEB-2001
                      neurosis;
                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      regulator
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                    Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB 4; I
Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                   Ewe colostrinin peptide fragment B-7.
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                                                                                                                        AAB59322 standard; peptide; 15
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DLEMPVLPVEPFPFV 15
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Best Local Similarity
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AAB72250;

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Boldogh

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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. It is classified as having a cytokine in a cell by contact with an immunological regulator, where the cytokine in a cell by contact with an immunological regulator, where the coll is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions of fective to induce a cytokine; modulating an immune response in a patient by administering an immunological regulator under conditions ceffective to induce a cytokine; where the immunological regulator is administered topically or as part of a distary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting blood cells with a blood cell regulator, where the blood cells are present in a cell culture or an organism, are mammalian or human, and where the blood cells are increased in number or differentiated; and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colostrinin; colostrum; immunomodulator; cardiovascular;
blood cell regulator; cytokine inducer; beta-casein; human.
                                                                                                                                                            Length 15;
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100.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 0;
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                     Sequence 15 AA;
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                                                                                                                  use ot colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                                                                                                                                                        The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neural cell differentiation; neural cell regulator; colostrinin peptide; neural cell formation; proline-rich polypeptide aggregate; colostrum; neural cell treatment.
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100.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA014581 standard; peptide; 15 AA.
                                                                                                                                                                                                                              Claim 6; Page 21; 35pp; English.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                              WPI; 2001-226545/23.
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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Modified-site

21-FEB-2002

analog

Unidentified

27-MAY-2002

AA014581;

RESULT 5 AAO14581 ID AAO

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The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, corgan, or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/ after a premature birth or normal birth, preventing/delaying aging in a premature birth or normal birth, preventing/delaying aging in a premature birth or normal birth, preventing/delaying aging species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stress regulator is not present. The modulation of oxidative stress results in chanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
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method for modulating blood cell proliferation in a patent. A claimed cytokine-inducing composition comprises a pharmaceutical carrier and active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10
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                                                                                                                                                        100.0%; Score 81; DB 5; I
100.0%; Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colostrinin constituent peptide #5.
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                                                                                                                                                                                                                                                                                                                                                                               AAE20232 standard; peptide; 15 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of colostrinin for e.g. modulating an intracellular signaling molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                          modulator; colostrinin; intracellular signaling-molecule modulator; 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor; 4HNE-protein adduct formation reduction; 44HNE-mediated glucathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide
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                                                                                                     Score 81; DB 5; I
Pred. No. 1.4e-05;
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                                                                                                                                       0; Mismatches
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STANTON J G.
GEORGIADES J A.
HUGHES T K.
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                                                                     Sequence 15 AA;
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(HUGH/)
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Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a peptide that can be recovered from ovine colostrinin using the method of the invention. The invention provides a method for the recovery of peptides (especially colostrinin) from colostrim in substantially pure, biologically active form and in high yield. The method involves mixing the colostrum with an alcohol to cortaining higher molecular weight caselins and other proteins. Best containing higher molecular weight caselins and other proteins. Best results are obtained using methanol or ethanol of at least 80%, and preferably up to 100%, purity. The alcohol phase is then separated from the precipitate, and the colostrinin is separated from the alcohol. Preferably by evaporation, to form a colostrinin-rich phase, which is recovered. A precipitation agent, such as ammonium sulfate, may be added ither to the alcohol phase or, preferably, to the colostrinin-rich phase to induce precipitation of the colostrinin peptides. The method is generally applicable to the separation of peptides from fluids containing higher molecular weight proteins, lipids, carbohydrates and/or nucleic acids. In an example from the invention, the antigenic profile of containing methods was determined by ELISA using antibodies prepared against a synthetic peptides; including a peptide having the present sequence
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or reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and recovering alcohol phase.
                                                                                                                                                                        Gaps
                                                                                                                                                                        ö
                                                                                                                             Length 15;
                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colostrum; colostrinin; sheep; peptide purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polanowski A, Wilusz T, Kruzel ML;
                                                                                                                             Score 81; DB 8; 1
Pred. No. 1.4e-05;
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 15; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                       Ä
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0
                                                                                                                                                                                                                                                                                                                                                                     ADS74398 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-2003; 2003GB-00005552.
08-MAR-2004; 2004GB-00005190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2004; 2004WO-GB001014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (denoted antigen class B-8).
                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                           1 DLEMPVLPVEPFPFV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovine colostrinin peptide
                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                 1 DLEMPVLPVEPFPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-677519/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004081038-A1.
                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georgiades JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries.
                                                                                                                                                                                                                                                                                                                                                                                                                ADS74398;
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ADS74398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system development of a child's immune system, as a distart such as child's immune system, as a distary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                   Gaps
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  Length 15;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Ewe colostrinin peptide fragment derived sequence #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 81; DB 4; I 100.0%; Pred. No. 1.5e-05; Live 0; Mismatches 0;
100.0%; Score 81; DB 8; I 100.0%; Pred. No. 1.4e-05;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE07187 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                           AAB59352 standard, peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 27; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000; 2000WO-GB002128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99GB-00012852
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                                                                                                                                             1 DLEMPVLPVEPFPFV 15
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                                                                                            1 DLEMPVLPVEPFPV
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nes 15; Conserv
Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-2000
                                                                                                                                                                                                                                                                                                                         AAB59352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis sp.
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Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacteriai; Parkinson's disease; Alzheimer's disease; mental disorder; food additive; central nervous system disorder; neurodegenerative disorder; weight loss; central nervous system disorder; neurosis; cachexia; motor neuron disease;

beta-amyloid plaque; psychosis; neurosis; cachexia; motor acquired immunological deficiency; neurological disorder; antiviral; cyclic.

/note= "N-terminal acetyl; this residue forms a cyclic linkage with Pro found at the C-terminal end"

Location/Qualifiers

Key Modified-site

Synthetic.

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The invention relates to colostrinin peptide fragments which are useful, inter alia, in the treatment of chronic disorders of the immune system and the central nervous system. Colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., Alzheimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g., psychosis and cheases characterised by the presence of betaneurosis, in acquired immunological deficiencies, chronic bacterial and viral infections and diseases characterised by the presence of betanewyloid plaques and as a dietary supplement for babies, small children, adults and senile persons, who have been subjected to chemotherapy or have suffered from cachesia or weight loss due to the chronic disease. Colostrinin peptides are also used as food additives and as an auxillary withdrawal treatment for dumy additers, after a period of detoxification and in persons dependent on stimulants. Colostrinin peptides are used to prepare antibodies and to treat enctional disturbances, e.g. emotional disturbances of psychiatric patients in a state of depression. These colostrinin peptides improves the development of immune system in a new born child and to correct the immunological deficiencies in a child. The present sequence is colostrinin peptide 3 related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                   Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial; Parkinson's disease; Alzheimer's disease; mental disorder; food additive; central nervous system disorder; neurodegenerative disorder; weight loss; beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease; acquired immunological deficiency; neurological disorder; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 4; Length 10;
Pred. No. 0.041;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; bred
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 15; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-2000; 2000GB-00001825.
                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2001; 2001WO-GB000329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
Best Local 10; Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                          Colostrinin peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488775/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PVLPVEPFPF
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                                                                                                                                                                                                                                                                                WO200155199-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georgiades JA;
                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                          02-AUG-2001
                                                                                                                                                                                               antiviral.
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Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.

(REGE-) REGEN THERAPEUTICS PLC.

WPI; 2001-488775/53.

Georgiades JA;

26-JAN-2001; 2001WO-GB000329. 26-JAN-2000; 2000GB-00001825

WO200155199-A1

02-AUG-2001

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The invention relates to colostrinin peptide fragments which are useful, inter alia, in the treatment of chronic disorders of the immune system and the central nervous system. Colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., Alzheimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g. psychosis and neurosis, in acquired immunological deficiencies, chronic bacterial and viral infections and diseases characterised by the presence of beta-amyloid plaques and as a dietary supplement for babies, small children, amyloid plaques and as a dietary supplement for babies, small children, have suffered from cachexia or weight loss due to chemotherapy or have suffered from cachexia or weight loss due to the chronic disease. Colostrinin peptides are also used as food additives and as an auxillary withdrawal treatment for drug addicts, after a period of detoxification prepare antibodies and to treat emotional disturbances, e.g. emotional disturbances of psychiatric patients in a state of depression. These
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colostrinin peptides improves the development of immune system in a new born child and to correct the immunological deficiencies in a child. The present sequence is modified colostrinin cyclic peptide #3 related to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%; Score 51; DB 4;
100.0%; Pred. No. 0.33;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB64957 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 8; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVLPVEPFP
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Modified colostrinin cyclic peptide #3.

(first entry)

06-NOV-2001

BXAXAX

AAE07197;

AAE07197 standard; peptide; 10 AA.

RESULT 12

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New isolated nucleic acids encoding any of about 1700 Methanopyrus kandleri proteins, and the encoded proteins, useful as a medicaments or
                                                                                                                                                         Hyperthermophile Methanopyrus kandleri protein #1194.
                                                                                                                                                                                                     hyperthermophile; protein stability enhancement; protein activity enhancement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; SEQ ID NO 1194; 1023pp; English.
                     ADM26588 standard; protein; 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-2002; 2002US-0361742P.
14-MAY-2002; 2002US-0380423P.
16-SEP-2002; 2002US-0410974P.
                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2003; 2003WO-US006664
                                                                                                                20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slesarev AI, Pavlov A,
                                                                                                                                                                                                                                                                               Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-748383/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADM27081
                                                                                                                                                                                                                                                                                                                           WO2003076575-A2
                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2003
                                                                 ADM26588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MALY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FIDE-)
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                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynucleotide, or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contexting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotide and encoded genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell respensation. Membrane proteins, disease-related proteins, disease-related proteins, creamcription-related proteins, disease-related proteins, disease-related proteins, diseases.

The croding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed by the specification, but is based on sequence information supplied by the European Patent Office.
                                                                                       Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration,
cell regeneration, membrane protein, signal transduction-related protein,
transcription-related protein, osteoporosis, neurological disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 7; Length 232;
Pred. No. 28;
2; Mismatches 2; Indels
                                              Human protein encoded by clone PROST20054660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELL-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                      28-MAR-2002; 2002EP-00007401.
                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as targets of gene therapy
04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J, Isono Y,
Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-450961/43.
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                                                                                                                                                                 cancer; tumour.
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                         EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J,
Seki N, Yosh
                                                                                                                                                                                                                                                                                                     07-MAY-2003.
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Kozyavkin S;

Pavlova N,

FIDELITY SYSTEMS INC. MALYKH A.

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The invention comprises the amino acid sequence of proteins from the hyperthermophile Methanopyrus kandleri, the invention also comprises the complete genome from Methanopyrus kandleri. The Methanopyrus kandleri proteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus kandleri genome is useful in a variety of diagnostic and analytical methods. The present amino acid sequence represents a Methanopyrus kandleri protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                Length 180;
                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes immunogenic protein #21282.
                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                              ore 46; DB 7 red. No. 42; Mismatches
                                                                                                                                                                                                                  Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU60386 standard; protein; 55 AA.
                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                  56.8%;
                                                                                                                                                                                                                                                                                                     2 LEMPVLPVEPFPFV 15
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                                                                                                                                                                                                                                                                                                                                               29 LECSVLPVPPEPFV 42
                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
                                                                                                                                                                          Sequence 180 AA;
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RESULT 14

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by content prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by constitutions. The disorders include SAPHO syndrome (synovitis, acne, bustulosis, hypertosis and osteonyalitis), uveitis and endophthalmitis. Compared in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies compactific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contame linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                            Mitcham JL, Wang SS, Bhatia A;
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.6%; Score 45; DB 4; Length 55; 63.6%; Pred. No. 17; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 21581; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                     21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                             20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                            Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-616774/71.
N-PSDB; AAS59609.
                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55 AA;
                     WO200181581-A2
                                                                01-NOV-2001.
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4 MPVLPVEPFPF 14 ઠ 유

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Gaps ö

23 LPVLPQSPFPY 33

Search completed: April 12, 2005, 08:18:21 Job time : 86 Becs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 12, 2005, 07:49:30; Search time 17.5909 Seconds (without alignments) 63.654 Million cell updates/sec Run on:

US-10-691-330-5 81 1 DLEMPVLPVEPFPFV 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA: Database :

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		۵			SUMMAKIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
	81	100.0	15	4	US-09-641-803-5	'	
8	45	55.6	803	4	US-09-252-991A-30479	ĕ	
e	44		259	4	US-09-328-352-4873	Sequence 4873, Ap	
4	42	51.9	148	4	US-09-270-767-56845	Sequence 56845, A	
ഗ	42		218	4	US-09-538-092-178		
9	42		242	4	US-09-252-991A-28361	Sequence 28361, A	
7	42		261	4	US-09-270-767-59826	59826,	
80	42	51.9	330	4	US-09-270-767-41611		
6	42	51.9	453	4	US-09-270-767-44397	44397,	
10	42		467	4	US-09-270-767-61831		
11	42	51.9	704	4	US-09-270-767-46262		
12	41.5	51.2	78	4	US-09-513-999C-5875		
13	41.5	51.2		4	US-09-461-325-456	456,	
14	41.5	51.2		4	US-10-012-542-456	456,	
15	41.5	51.2		4	US-10-115-123-456		
16	41	50.6		4	US-09-902-540-15704		
17	41	50.6		4	-09-902		
18	41	50.6	-	4	US-09-248-796A-15522	15522	
19	40	49.4		4	•	22	
20	40	49.4		m	-09-527	2, Ag	
21	40	49.4		4		N	
22	40	49.4		4	US-09-489-039A-9575	957	
23	6.	48.8	4	<b>♂</b>	US-09-902-540-10492	104	
24	39.5	48.8	651	4	US-09-932-678-2	'n	
25	39	48.1		4	US-09-198-452A-211	211	
56	39	48.1	220	4	US-09-438-185A-194		
27	39	48.1	263	4	US-09-902-540-15616	156	

Sequence 374, App Sequence 22, App1 Sequence 129, App1 Sequence 20775, App Sequence 6, App1 Sequence 1517, App1 Sequence 1629, App1 Sequence 1629, App Sequence 1639, App Sequence 1689, App Sequence 19914, Appli Sequence 1689, App Sequence 1689, Appli Sequence 1898, Appli	Sequence 17298, A Sequence 7220, Ap Sequence 7221, Ap
US-09-149-476-374 US-09-593-623-22 US-09-553-22 US-09-558-092-1299 US-09-252-991A-20775 US-07-211-796-6 US-07-211-796-6 US-07-211-796-8 US-09-248-796A-15517 US-08-945-771-2 US-09-902-540-16293 US-09-248-796A-14914 US-09-270-767-40882 US-09-270-767-40882 US-09-270-767-5698 US-09-270-767-5698	US-09-248-796A-17298 US-09-949-016-7220 US-09-949-016-7221
<b>ਰਾਨੀ ਰਾਹਾਰੀ ਜਿਹਾਰੀ ਦੀ ਦੀ ਦੀ</b>	444
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	8 8 8 8 8 8
0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 4 4 5 5 4 5

## ALIGNMENTS

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Sequence 5, Application US/09641803

Patent No. 6500798

GENERAL INFORMATION:

APPLICANT: STANTON, G. John

APPLICANT: BOLDOGH, 16tvan

TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

FILE REFERENCE: 265.00220101

CURRENT APPLICATION NUMBER: US/09/641,803

CURRENT APPLICATION NUMBER: US/09/641,803

CURRENT APPLICATION NUMBER: 00/149,310

PRIOR FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 5

LENGTH: 15

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels

; 0

1 DLEMPVLPVEPFFV 15 1 DLEMPVLPVEPFPV 15 셤 ò

RESULT 2 US-09-252-991A-30479

Sequence 30479, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASERCISION ASERCIS OF SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUGUSTS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18

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Sequence 38361, Application US/09252991A

Sequence 38361, Application US/09252991A

Pacent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28361

LENGTH: 242
                   GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
TILLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR PLICATION NUMBER: 60/127,352
PRIOR PLICATION NUMBER: 60/178,965
PRIOR PLING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 178
LENGTH: 218
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Batent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (0) ... (0) OTHER INFORMATION: Polypeptide Accession Number YDR236C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 42; DB 4;
58.3%; Pred. No. 55;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 42; 53.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLEMPVLPVEPFPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 bleipaopgepepeuv 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.9
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EMPVLPVEPFPF 14
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                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KBY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-28361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4873
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56845
LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                  Score 45; DB 4; Length 803;
Pred. No. 69;
3; Mismatches 4; Indels
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Pred. No. 30;
3; Mismatches 2; Indels
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Pred. No. 33;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56845, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4873, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-538-092-178 Sequence 178, Application US/09538092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56845
                                                                                           ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30479
                                                                                                                                                                  Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      318 DAEPPVVPVQVLPYV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%;
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166 MVVRPVDPYPFI 177
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Best Local Similarity 58.3
Matches 7; Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 30479
LENGTH: 803
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Best Local Similarity
Matches 6; Conserva
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                                                                          TYPE: PRT
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Length 242;

Matches

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TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 42.3%
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.5.
Best Local 6; Conservative
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                                                                                                                                                                                                                                                                                                                                         US-09-270-767-41611

Sequence 41611; Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

TILLE OF INVENTION:

FILLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 41611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7128-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 44397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.1e+02;
3; Mismatches 5; Indels
                                                                                                                                                               DB 4; Length 261;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%; Score 42; DB 4; Length 330; 42.9%; Pred. No. 77;
                                                                                                                                                                                                   5; Indels
                                                                                                                                                               Score 42; DB Pred. No. 60; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44397, Application US/09270767 Patent No. 6703491
                                                                                     TYPE: PRT : ORGANISM: Drosophila melanogaster US-09-270-767-59826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                               51.9%;
42.9%;
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188 DAQQPAVPMAPMPF 201
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                 NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59826
LENGTH: 261
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Best Local Similarity 42.5-
Best Local 6; Conservative
                                                                                                                                                                                                 6; Conservative
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Matches 6; Conservative
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Best Local Similarity
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US-09-270-767-44397
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Sequence 61831, Application US/09270767

Sequence 61831, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE FILE NETRINGER FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 61831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46262, Application US/09270767

Patent No. 6703491

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46262
LENGTH: 704
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Patent No. 6783961

Batent No. 6783961

APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Sylvassed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT PLING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%; Score 42; DB 4; Length 4b, 42.9%; Pred; No. 1.18+02; "...marrhes 5; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 42; DB 4; 42.9%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-61831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-46262
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RESULT 10

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2 LEMPVLP----VEPFP 13
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17 LEVPILPTHHLLIHPFP 33
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17 LEVPILPTHHLLIHPFP 33
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 47.1
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-10-115-123-456
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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| Sequence 456, Application US/10012542
| Patent No. 6627741
| GENERAL INFORMATION: 4
| TITLE OF INVENTION: 94 Human Secreted Proteins |
| FILE REFERENCE: P2029P1 |
| CURRENT APPLICATION NUMBER: US/10/012,542 |
| CURRENT FILING DATE: 2001-12-12 |
| PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/089,507 |
| PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14 |
| PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507 |
| PRIOR PLILING DATE: EARLIER RELING DATE: 1998-06-16 |
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
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                                                                                                                                                                                 DB 4; Length 78;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE KEFERENCE: PZOZBYL

CURRENT PEDLICATION NUMBER: US/09/461,325A

CURRENT FILING DATE: 1999-12-14

BEALLIER APPLICATION NUMBER: PCT/US99/13418

EARLIER PILING DATE: 1999-06-15

EARLIER PEDLICATION NUMBER: 60/089,507

EARLIER FILING DATE: 1998-06-16

EARLIER FILING DATE: 1998-06-16

EARLIER FILING DATE: 1998-06-16

EARLIER PEDLICATION NUMBER: 60/089,509

EARLIER PILING DATE: 1998-06-16

EARLIER PEDLICATION NUMBER: 60/089,510

EARLIER PEDLICATION NUMBER: 60/089,510

EARLIER PEDLICATION NUMBER: 60/080,112

EARLIER PEDLICATION NUMBER: 60/080,113

EARLIER PEDLICATION NUMBER: 60/090,113

EARLIER PEDLICATION NUMBER: 60/090,113

EARLIER PELLING DATE: 1998-06-22

SOFTWARE: PAPELICATION NUMBER: 60/090,113

EARLIER PELLING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PAPENICATION NUMBER: 60/090,113
                                                                                                                                                                              Query Match 51.2%; Score 41.5; I
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches
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Patent No. 6475753
GENERAL INFORMATION:
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17 LEVPILPTHHLLIHPFP 33
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17 LEVPILPTHHLLIHPFP 33
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Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                 ORGANISM: Homo sapiens
US-09-513-999C-5875
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; ORGANISM: Homo sapiens
US-09-461-325-456
SOFTWARE: Patent.pm
SEQ ID NO 5875
LENGTH: 78
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US-10-012-542-456
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Gaps
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-22
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-22
SOFTWARE: PALCHIER FILING DATE: 1998-06-22
SOFTWARE: PALCHIN VOF: 2.0
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Patent No. 6774216
Facent No. 6774216
FILE REFRENCE: P20209304D102
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
FRIOR FILING DATE: 1999-06-15
FRIOR FILING DATE: 1998-06-16
FRIOR FILING DATE: 1998-06-22
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Sequence 166092, Sequence 192065, Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 106, App

Sequence 12, Appl Sequence 32203, A Sequence 216454, Sequence 38710, A

Scoring table:

Searched:

Database

Result

Title: Perfect score:

Sequence:

OM protein

Run on:

8560, Ap 145459,

Sequence Sequence Sequence Sequence Sequence Sequence

12405,

Sequence 29, Appl Sequence 2, Appli Sequence 192, App Sequence 216458,

Sequence 104274, Sequence 137718, Sequence 42069,

Sequence

Sequence 10911,

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Sequence 5, Application US/10281652
Publication No. US20030091606A1
GENERAL INFORMATION:
APPLICANT: BUGHES, Thomas K.
APPLICANT: HUGHES, Thomas K.
TITLE OF INVENTION: USE OF CCLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: WALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
TITLE OF INVENTION: USE OF CCLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: UNDER: US/10/281,652
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/09/641,803
PRIOR PILING DATE: 1000-08-17
PRIOR PELING DATE: 1099-08-17
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10.5-10-424-599-204279
10.5-10-424-599-204279
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10.5-10-437-963-171233
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10.5-10-437-963-112405
10.5-10-437-963-112405
10.5-10-437-963-1147-192
10.5-10-437-963-1147-192
10.5-10-437-963-1137718
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ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 15
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Best Local Similarity 100.
Matches 15, Conservative
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Sequence 58864, A
Sequence 3111, Ap
Sequence 77182, A
Sequence 254766,
Sequence 254766,
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                                                                                                                                                                                                   April 12, 2005, 07:49:30 ; Search time 46.5 Seconds (without alignments) 107.096 Million cell updates/sec
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Sequence 1
Sequence 4
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6/prodate/1/pubpad/USO_NEW PUB.ppp: *
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6/prodate/1/pubpad/USOT NEW PUB.ppp: *
6/prodate/1/pubpad/USOT NEW PUB.ppp: *
6/prodate/1/pubpad/USOT NEW PUB.ppp: *
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-691-330-5

US-10-182-110-3

US-10-425-114-58864

US-10-104-047-3111

US-10-282-122A-77182

US-10-437-963-108040

US-10-424-599-284766

US-10-424-599-24024

US-10-424-599-146697

US-10-369-146697

US-10-369-146697

US-10-12-542-456
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1: /cgn2_6/ptodata/1/pubpaa/U2
2: /cgn2_6/ptodata/1/pubpaa/P3
3: /cgn2_6/ptodata/1/pubpaa/U4
4: /cgn2_6/ptodata/1/pubpaa/U5
5: /cgn2_6/ptodata/1/pubpaa/U6
6: /cgn2_6/ptodata/1/pubpaa/U9
7: /cgn2_6/ptodata/1/pubpaa/U9
8: /cgn2_6/ptodata/1/pubpaa/U9
9: /cgn2_6/ptodata/1/pubpaa/U9
9: /cgn2_6/ptodata/1/pubpaa/U9
9: /cgn2_6/ptodata/1/pubpaa/U9
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Maximum Match 100%
Listing first 45 symmaries
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Maximum DB seq length: 200000000
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Match Length DB
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Bublication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESERRCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REPERBENCE:

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT PILING DATE: 2002-03-25577

FRIOFF, PRIOFF, PRIOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 104;
APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabaska, Jack E.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molec, TITLE OF INVENTION: Plants and Uses Thereof for Plant Implement APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 58864

LENGTH: 104

TYPE: PPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: 700431848_FLI.pep US-10-425-114-58864
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209 KFPVLPVHPWPF 220
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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US-10-104-047-3111
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Matches 8; Conserv
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                        APPLICANT: Boldogh, 18 to van APPLICANT: Boldogh, G. John APPLICANT: Boldogh, G. John APPLICANT: Boldogh, G. John APPLICANT: Boldogh, Jerzy A. APPLICANT: Georgiades, Jerzy A. APPLICANT: Hughes, Thomas K., Jr. APPLICANT: Kruzel, Marian TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE FILE REPERENCE: 265.00390101
CURRENT PILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: US 60/420,369
PRIOR FILING DATE: 2002-10-22
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, OTHER INFORMATION: Truncated version of a peptide found in colostrinin
US-10-182-110-3
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APPLICANT: Reden Therapeutics plc
APPLICANT: Recorgiades, Jerzy A
TITLE OF INVENTION: Peptide Fragments of Colostrinin And Their Use
FILE REPERBNCE: AAT-1412
CURRENT APPLICATION NUMBER: US/10/182,110
CURRENT FILING DATE: 2003-04-21
PRIOR FILING DATE: 2000-01-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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100.0%; Pred. No. 0.047;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Synthetic Peptides US-10-691-330-5
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Publication No. US20040171553A1
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SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 15
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial
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Sequence 58864, Application US/10425114; Publication No. US20040034888A1

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Gaps

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Best Local Similarity 47.4%; Pred. No. 58; Matches 9; Conservative '2; Mismatches
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Publication No. US20040031072A1
                                                                                                             ---FPFV 15
                                                                                                                                                  | || || :|: | ||||| 75 DAPMPEIPIHPPPPVFPFV 93
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77.8%;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 77.8
7, Conservative
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
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PRIOR PLILING DATE: 2000-03-21

PRIOR PELICATION NUMBER: 60/206,848

PRIOR PELICATION NUMBER: 60/206,848

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27

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PRIOR PLING DATE: 2000-10-29

PRIOR PILING DATE: 2000-10-29

PRIOR PLING DATE: 2000-10-3-18

PRIOR PLING DATE: 2000-10-10-18

PRIOR PRIOR PLING DATE: 2000-10-10-18

PRIOR PRIOR PRIOR PRIOR DATE: 2000-10-10-18

PRIOR PRIOR PRIOR PRIOR DATE: 2000-10-10-18

PRIOR PRIOR PRIOR PRIO
                                                                     APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 108040
LENGTH: 135
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Publication No. US20040123343A1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yngwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bradzuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLEMPVLPVEPFPFV 15
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   Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Vibrio cholerae
US-10-282-122A-77182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                    Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-437-963-108040
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Sequence 2840424, Application US/10424599
Sequence 2840404, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Zou Yihua
APPLICANT: Zo
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Royalic David K
APPLICANT: Show I thus
APPLICANT: Con Youngwei
TITLE CP INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
SEQ ID NOS: 285684
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Pred. No. 2e+02;
1; Mismatches 1; Indels
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US-10-424-599-254766
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US-10-424-599-284024
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Pred. No. 57;
1; Mismatches 6
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RESULT 10

54.3%; Score 44; DB 16; Length 135;

Query Match

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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERBYCE: 38-10(52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT APPLICATION NUMBER: US/60/369, REAL PRIOR APPLICATION NUMBER: US/60/360,039 PRIOR FILING DATE: 2003-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 18781 LENGTH: 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456, Application US/10012542

Sequence 456, Application US/10012542

Publication No. US20030044851A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 00/461,325

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PRILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER PLILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFFWARE: PATEUR PLING DATE: EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFFWARE: PATEUR PLANCENT.
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Pred. No. 4e+02;
2; Mismatches 2; Indels
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Pred. No. 86;
3; Mismatches 1;
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TITLE OF INVENTION: 94 Human Secreted Proteins
PILE REFERENCE: PZ029630APLD2
CURRENT APPLICATION NUMBER: US/10/115,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456, Application US/10115123; Publication No. US20030065151A1; GENERAL INFORMATION:
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.9%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-10-369-493-18781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 PIMPVMPFPDV 374
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-012-542-456
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Sequence 144697, Application US/10424599

Bublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: Expericant: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5323)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 144697

LENGTH: 249
                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 174
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Pred. No. 1.5e+02;
5; Mismatches 0; Indels
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US-10-424-599-144697
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US-10-424-599-204286
                                               Sequence 204286, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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51.9%; 54.5%;

Query Match
Best Local Similarity 54.5
Matches 6; Conservative

TYPE: PRT ORGANISM: Glycine max

1 DLEMPVLPVEP 11 ::::||:|||| 77 NIDIPVIPVEP 87

ò 셤 US-10-424-599-144697

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Sequence 18781, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Salter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
RESULT 12
US-10-369-493-18781
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Best Local Similarity 80.0 Matches 8; Conservative

Query Match

ORGANISM: Glycine max

FEATURE:

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2002-04-04

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Squence 20479, Application US/10424599

Fublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 204279
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| NAME/KDY: unsure
| LOCATION: (1)..(88)
| OTHER INFORMATION: unsure at all Xaa locations
| FEATURE:
| FEATURE:
| OTHER INFORMATION: Clone ID: PAT_MRT3847_26491C.1.pep
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PRIOR APPLICATION NUMBER: PCT (1999/13418)
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-16
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-12
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PARCHIN Ver. 2.0
SEQ ID NO 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.5;
Pred. No. 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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77 NIDIPVIPIEP 87
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ORGANISM: Homo sapiens
US-10-115-123-456.
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ORGANISM: Glycine max
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                                                                  April 12, 2005, 07:49:31; Search time 10.7727 Seconds (without alignments) 133.973 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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H82264
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AB1213
CC7736
S06869
H86514
G75055
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                             1 DLEMPVLPVEPFPFV 15
                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                      US-10-691-330-5
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1504
503
973
1421
266
266
360
435
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                      Title:
Perfect score:
                                                                                                                                                                       Scoring table:
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                                                OM protein
                                                                                                                                               Sequence:
                                                                                                                                                                                                           Searched:
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                                                                       Run on:
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No.
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DB 2; Length 446;

55.6%; Score 45;

Query Match

Gaps

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Indels

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R;Richardson, M.P.; Braybrook, C.; Tham, M.; Moore, G.E.; Stanier, P. Gene 206, 145-150, 1998
A;Ritle: Molecular cloning and characterization of a highly conserved human 67-kDa lamins A;Reference number: JG6530; MUID:98121324; PMID:9461426
A;Accession: JG6530
A;Status: conceptual translation of pseudogene
                                                                                                                                            A,Accession: S54532
A,Molecule type: DNA
A,Residues: 1-218 <-COLINICAGE TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-295 <RIC>
A,Experimental source: brain
C,Comment: No evidence could be found that this intronless gene sequence is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 28-Aug-1998 #sequence_revision 28-Aug-1998 #text_change 28-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 42; DB 2; Length 218; 53.3%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: SGD:S0002644
A, Map position: 4R
C, Feywords: transmembrane protein
F, F-20/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laminin receptor processed pseudogene LAMRLS - human
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R;McMurray, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z19871
A;Accession: T24298
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 28;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
C;Accession: S54532
R;Oliver, K.; Harris, D.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: clone T01E8
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 53.33
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  formylmethanofuran dehydrogenaee (tungsten) chain B homolog (fwdB-2) - Archaeoglobus full Cippecies: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69490
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R;KLenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.K.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: A69280; MUID:98049343; PMID:9389475
A;Reterence number: A69280; MUID:98049343; PMID:9389475
A;Reterence number: A69280; MUID:9804936; MID:92689293; PIDN:AAB89332
C;Superfamily: formylmethanofuran dehydrogenase (molybdenum; molybdenum; molybdopterin
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T24600
hypotherical protein T08D2:8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24690
R;McMurray, A.
Submitted to the EMBL Data Library, March 1997
A;Accession: T4690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 1-556 < WIL>
A;Mcseque: type: DMA
A;Residues: 1-556 < WIL>
A;Residues: 1-556 < WIL>
A;Experimental source: clone T08D2
C;Genetics:
A;Gene: CESP:T08D2.8
A;Introns: 5/1; 54/3; 80/3; 255/3; 307/3; 352/3; 479/1
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N;Alternate names: hypothetical protein YD8419.03c
C;Species: Saccharomyces cerevisiae
C;Species: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
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Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 2; Indels
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Pred. No. 29;
4; Mismatches 1; Indels
                                                         Indels
                                                         3,
                    Pred. No. 15;
4; Mismatches
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Best Local Similarity 54.5%;
Matches 6; Conservative
                nilarity 53.3%;
Conservative
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76 DLEVPNLELEAFPYL 90
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350 EIPVIQIDPFP 360
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443 PVAPVKPKPFV 453
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                    Best Local Similarity
Matches 8; Conserv
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S54532
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A; Cross_references: UNIPROT: 022069; EMBL: Z48809; PIDN: CAA88744.1; GSPDB: GN00020; CESP:TO
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A,Map position: Xq21.3
A,Introns: #status absent
C,Keywords: brain; glycoprotein; laminin binding; pseudogene; receptor
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                                                            4; Length 295;
                                                                                               Indels
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R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Poco, Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A;Reference number: Z16030; MUID:95024047; PMID:7937893
                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-696 <WAK>
A;Cross-references: UNIPROT:P52733; EMBL:D17510; NID:g529643; PIDN:BAA23472.1; PID:g2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T17426
Kyndramedi, H.; Shafiee, A.
Bur. J. Biochem. 256, 528-534, 1998
A;Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressan
A;Reference number: Z18779; WUID:98451508; PMID:9780228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: required during the biosynthesis of the immunosuppressant FK506 for the ar C; Superfamily: Mycobacterium tuberculosis mbtE protein; acetate-CoA ligase homology; acy C; Keywords: carrier protein; phosphopantetheine; phosphoprotein F; 5395-Momain: acetate-CoA ligase homology AGL>
F; 599-1067/Domain: acetate-CoA ligase homology AGC>
F; 9103-1067/Domain: acyl carrier protein homology ACC>
F; 1031/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                      DNA-directed RNA polymerase (EC 2.7.7.6) beta'-1 chain - Japanese black pine chloroplast C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
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A;Experimental source: strain MA6548
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A;Variety: strain MA6548
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: chloroplast
A;Note: intron positions not resolved (incomplete sequence)
C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-1
C;Keywords: chloroplast; nucleotidyltransferase; transcription
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53.3%; Pred. No. 1.8e+02;
tive 2; Mismatches 5;
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75;
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1; Mismatches
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285 LPVLPPEPRPIV 296
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nes 8; Conserv
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                A; Accession: T07447
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                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aldehyde dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)
Cispecies Nostoc sp. PCC 7120
A;Note: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2433
K;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sassamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Reference Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-473 <KUR>
A;Residues: 1-473 <KUR>
A;Cross-references: UNIPROT:Q8YMB2; GB:BA000019; PIDN:BAB76721.1; PID:g17134160; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all:022
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1942
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. S.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MuID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8YXW8; GB:BA000019; PIDN:BAB73046.1; PID:g17130435; GSPDB:0
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein all1089 (imported) - Nostoc sp. (strain PCC 7120)
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                                                                                             Length 367;
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Pred. No. 49;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 448
                                                                                                                                                   3; Indels
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                                                                                          Score 42; DB Pred. No. 36; 1; Mismatches
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Pred. No.
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                                                                                       Query Match 51.5
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
A, Map position: 2
A, Introns: 48/2; 200/2; 254/3
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365 PIMPVMPFPDV 375
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ELPLLPVDPY 107
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ilarity 50.0%;
Conservative
                                                                                        2 LEMPVLPVEPFP 13
     Best Local Similarity
Matches 6; Conserval
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A, Molecule type: DNA
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-503 <KUR>
A;Cross-references: UNIPROT:Q0UHS9; GB:AE007869; PIDN:AAK86411.1; PID:g15155545; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein KIAA0560 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 0.7 Peb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00333 R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res; S, 31-39, 1998 A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: Z14086; MUD:98290545; PMID:9628581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-973 <WOO>
A;Cross-references: UNIPROT:Q9USL3; EMBL:AL109736; PIDN:CAB52155.1; GSPDB:GN00068
A;Experimental source: strain 972h-; cosmid c18B5
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A;Cross-references: UNIPROT:O60306; EMBL:AB011132; NID:d1185402; PIDN:BAA25486.1
A;Experimental source: brain; clone HH1648
C;Genetics:
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J. Bubmitted to the EMBL Data Library, July 1999
A;Reference number: Z21978
A;Accession: T41201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 503;
Pred. No. 75;
3; Mismatches 5; Indels
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A;Molecule type: mRNA
A;Residues: 1-1421 <NAG>
                                                                                                                                                                                                                                                                                                       A,Gene: AGR C 1065
A,Map position: circular chromosome
C,Superfamily: glucose-6-phosphate dehydrogenase
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A;Gene: SPBC18B5.08c
Apane: SPC18B5.08c
C;Superfamily: isoleucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.6%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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DMSSQIIPVEPFDCV 26
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Matches 7; Conserv
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- Agrobacterium tumefacier
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-266 <KUR>
A;Gross-references: UNIPROT:Q8U9W6; GB:AE008689; PIDN:AAL44421.1; PID:g17742021; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iter, E.W.
1,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
1,Reference number: AB2577; MUID:21608550; PMID:11743193
1,Accession: AG3000
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                                                                                                                                                                                                                                                                                1-acyl-sn-glycerol-3-phosphate acyltransferase plsC [imported] - Agrobacter:
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
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                       Indels
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Pred. No. 2.4e+02;
3; Mismatches 3;
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Pred. No. 5
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1264 LHLHIIPTEPFP 1275
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174 DLQVPVIPVAMHP 186
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 12, 2005, 07:49:31; Search time 71.1818 Seconds (without alignments) 107.909 Million cell updates/sec Run on:

US-10-691-330-5 81 1 DLEMPVLPVEPPFV 15 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score Match Le				
	Match Length DB	. qı	Description	
59.3	232 2	Q8NAJ2	O8naj2 homo sapien	
58.0	222 2	Q75DY2	Q75dy2 ashbya goss	
58.0	1766 2	P78584		
46 56.8	180 2	Q8TW43	Q8tw43 methanopyru	
46 56.8	935 2	Q7RZ84	O7rz84 neurospora	
	948 2	Q6M999	Q6m999 neurospora	
45 55.6	79 2	Q99ME4		-
	80 2	Q8LF16	Q81f16 arabidopsis	_
45 55.6	91 2	QBSBRS		
45 55.6	200 2	Q6GMA4	Q6gma4 xenopus lae	
	219 2	Q22140	Q22140 caenorhabdi	
	446 2	ОЭКТИВ		
	557 2	Q99L21	Q99121 mus musculu	
	599 2	QBC2N3	-	
	599 2	QBC3K9	mus	
	599 2	Q8C4X8	Bum	-
45 55.6	607 2	Q8BSP2	Q8bsp2 mus musculu	
	619 2	Q9H5Q7	Q9h5q7 homo sapien	
	668 2	Q9H5C7	Q9h5c7 homo sapien	
	772 2	О9ВГН1		
	902 2	Q8G762	Q8g762 bifidobacte	
	1307 2	Q9C093	Q9c093 homo sapien	
	1744 2	Q9R095		
44 54.3	191 2	Q6ACW3	Q6acw3 leifsonia,x	
44 54.3	428 2	Q6K6Z8		
44 54.3	593 2	Q7RN16		
44 54.3	638 2	Q75RZ6	Q75rz6 ciona intes	
44 54.3	656 2	Q754Q2	Q754q2 ashbya goss	
44 54.3	726 2	Q6G327	. Q6g327 bartonella	
3 53.1	388 2	Q9XTX7	Q9xtx7 caenorhabdi	
3 53.1	421 2	028350	O28350 archaeoglob	_

Q98r06 arabidopsis Q8wny2 o potassium Q91rv1 arabidopsis Q7dj10 anopheles g Q67r28 symbiobacte Q0378 saccharomyc Q9vyg4 drosophila Q94av8 arabidopsis Q88n4 pseudomonas Q22069 caenorhabdi Q8yxw8 anabaena sp Q6agj9 lalfsonia x Q69yg9 drosophila	
09SR06 KCH2_RABIT 09LKVI 07QJI0 067RZ8 RIFK YEAST 09VXG4 094AV8 022069 089N4 022069	Q9W5D6
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444 1161 681 157 200 218 232 265 367 448 448	469
5 6 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	51.9
4 0 4 4 4 4 4 4 4 4 4 4 4 4 6 6 7 0 0 0 0 0 0 0 0 0 0 0 0	42
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

# ALIGNMENTS

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[1]
SEQUENCE FROM N.A.
STRAIN=OR74A;
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                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=2320;
                                                             Transferase.
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                                                                                                   Query Match
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Q8TW43
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X MEDLINE-98268975; PubMed-9603849;
X FEDGINE-98268975; PubMed-9603849;
X FEDGINE-98268975; PubMed-9603849;
X Tacilture conditions control expression of the genes for aflatoxin and RT sterigmatocystin biosynthesis in Aspergillus parasiticus and A.

RT "Culture conditions control expression of the genes for aflatoxin and RT sterigmatocystin biosynthesis in Aspergillus parasiticus and A.

RT "Appl. Environ. Microbiol. 64:2275-2277 (1998).

REMBL, US2151; AAC25336.1; -...

R GO; GO:0006633; P:cofactor binding; IEA.

R GO; GO:0006633; P:metabolism; IEA.

R InterPro; IPR001727; Ac transferase.

R InterPro; IPR001737; Ac transferase.

R InterPro; IPR001633; Pspgnateth_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Fungi, Ascomycota, Pezizomycotina, Burotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5067;
                                                                                                                                                                             Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                             STRAIN=ATCC 10895;
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; ARO16815; AAS50662.1; -. AGD; ABL109W; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 47; DB 2; Length 222; 46.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                         AD Synth; 1.
25125 MW; 965B95DD257FB439 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     GO; GO:0008531; F:riboflavin kinase activity; IEA.
GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.
InterPro; IFR0025606; FBD Synth.
Pfam; PF01687; FAD Synth; 1.
ProDom; PD003662; FAD_Synth; 1.
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                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2004 (TrEMBLrel. 26, Polyketide synthase PKSL2. Name-pksL2;
                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLEMPVLPVEPFPFV 15
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            : ||||| |:||
209 KFPVLPVHPWPF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 46.7 tes 7; Conservative
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3 EMPVLPVEPFPF 14
                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus parasiticus.
                                                                                                                                                                                                                                                                                                                                                                                                           222 AA;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                    ORFNames=ABL109W;
                                                                                                                                                                                                                     NCBI_TaxID=33169;
                                                                                                                                                       ABL109Wp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                       Q75DY2
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                                                              RESULT 2
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Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
Sheherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Nataleov R.L., Wolf Y.I., Stetter K.O., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin B.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19 and amonophyly of archaeal methanogens.";
EMBL, Acolo411; AAM02407.1; -.
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                          58.0%; Score 47; DB 2; Length 1766; 60.0%; Pred. No. 1.6e+02; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f match 56.8%; Score 46; DB 2; Length 180; Local Similarity 71.4%; Pred: No. 20; 10; Conservative 0; Mismatches
                                                                                                                                                                                 1766 AA; 192067 MW; E20C4BF26F60671E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA; 19963 MW; 8935B0CADA923F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Uncharacterized membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
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Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; Ketoacyl-synt_C; 1.
Pfam; PF00550; PP-binding; 1.
PROSITE; PS50075; ACP DOMAIN; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        1340 DLEMPVLPLATMKYV 1354
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                                                                                                                                                                                                                                                                             Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                     1 DLEMPVLPVEPFPFV 15
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948 AA; 102502 MW; D53CFA84C8F6351C CRC64;
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Best Local Similarity
7; Conservē
                                                                 Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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    SEQUENCE
                                                  Query Match
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QBLF16;
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Q99ME4;
                                                                             Best Loc
Matches
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Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Rothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., A. Roy A., Foley K., Naylor J., Thomann M., Barrett R., Gnerre S., Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Barglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Lander E.S., Dunlap J., Freitag M., Apulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; Nature 0:0-0(203).

I. The Genome Sequence of the Filamentous Fungus Neurospora crassa.; Nature 0:0-0(203).

C. -! - SIMILARITY: Contains 1 SET domain.

EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Neurospora genome project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Contains 1 SET domain.
EMBL; BX908809; ZAF06059.1; --
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR011011; FYUE_PHD_ZnF.
InterPro; IPR001214; SET.
InterPro; IPR001214; SET.
DEFORES. DEFORES. DEFORES. DEFORES.
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                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AABX01000720; EAA28230.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR01111; FYVE_PHD_ZnF.
InterPro; IPR001214; SET.
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%; Score 46; DB 2; Length 935; 61.5%; Pred. No. 1.2e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 935 Aa, 101487 MW; FC41A43B126C4DAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein 29E8.260.
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809 DLRVPMPPVPPFP 821
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Best Local Similarity 61...
Best Local Similarity 61...
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SMART; SM00317; SET; 1
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Pfam; PF00856; SET; 1.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
4-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons; core eudicots; rosids, Surantophyta, Bassicales, Brassicacese, Arabidopsis.
                                                         Gaps
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     Length 948;
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 80;
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xie C., Yang Y., Yang Y., Cai D., Cheng G., Li G., Luo M Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF348365; AAK15769 J.
ERQUENCE 79 AA, 8994 WW; P884278152833C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Hypothetical protein.
SEQUENCE 80 AA, 8671 MW; BB1EF444B1A34E81 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
56.8%; Score 46; DB 2; Le
ilarity 61.5%; Pred. No. 1.2e+02;
Conservative 2; Mismatches 3;
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Pred. No. 12;
1; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%;
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                                                                                                                                                      809 DĽRVPMPPVPPFP 821
                                                                                                     1 DLEMPVLPVEPPP 13
                                                                                                                                                                                                                                                                                PRELIMINARY;
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EVPVLPLQPLP 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
7; Conserve
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Pfam; PF00252; Ribosomal L16;
PRINTS; PR00060; RIBOSOMALL16.
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InterPro; IPR005024; Snf7.
                                                                                                                                                                          initiative.";
Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                    167 DLELPEAPSEPLP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z35663; CAA84730.1;
PIR; T24429; T24429.
IntAct; Q22140; -.
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                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T. L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                          Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J., W. D., Matit R., Ronning C.M., Koo H., Fuji C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierwan W.C., Fraser C.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004136; AAM14912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     _.
CF45D5B3FB66192D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                          91 AA; 9870 MW;
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                                                                                                           08-5885;
01-JUN-2002 (TrEMBLrel, 21,
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 77.8
                                                                                                  PRELIMINARY;
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           13
                                    46
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             PVLPVEPFP
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PVIPTEPFP
                                                                                                                                                                Expressed protein.
Name=At2g02515;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and infial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2; Length 200;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormBase; WEGene00011412; T04A8.11.
WormBase; WEGene00011412; T04A8.11.
WormBep; T04A8.11; CE01066.
GO; GO:0005622; C:intraccllular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0006412; P:structural constituent of ribosome; IEA.
InterPro; IPR000114; Ribosomal_L16.
PF00.525; Ribosomal_L16; I.16.
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03357; SNF7; 1.
SEQUENCE 200 AA; 23326 MW; 5E71D569C7079769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein T04A8.11.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
A biachemko. L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Brange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NOD; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN fullength enriched library, clone:E430010H07 product:hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.6%; Score 45; DB 2; Length 557; 77.8%; Pred. No. 98; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003900; AAH03900.1; -.
MGD; MGI:1289164; DISErtd785e.
InterPro; IPR009378; DUF1032.
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SEQUENCE 557 AA, 63153 MW; 742CD81FEA32A7C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PVLPVEPFP 13
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Q8C2N3
                      TAPE SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=El Tor Ni6961 / Serotype Ol;
MEDLINE=20406833, PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=204068833, PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Daragil I.,
Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
Wekalanos J.J., Venter J.C., Fraser C.M.;
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 77;
4; Mismatches 3; Indels
           Hypothetical protein.
SEQUENCE 219 AA; 25360 MW; E22A1E0A573C3FDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 446 AA; 50713 MW; 85BDAC396E2EC45D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                       Score 45; DB;
Pred. No. 36;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                       55.6%;
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EMBL; AE004175; AAF94086.1;
PIR; H82264; H82264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%;
ilarity 53.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
D15Ertd785e protein.
Name=D15Ertd785e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DLEMPVLPVEPFPFV 15
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                                                                              Ouery Match
Best Local Similarity 63.0-
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CapK protein, putative.
OrderedLocusNames=VC0924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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21 LKLPVMPAEPF 31
                                                                                                                                                                                                                                                                2 LEMPVLPVEPF 12
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nes 8; Conserv
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AC 09912
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SEQUENCE FROM N.A.

STRAIN=C5/BL/6J; TISSUE=Kidney;
A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda K., Hayatsu N., Hiramocko K., Hiraoka T., Hirozane T.,
A Hoyashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINE-CYBL/GJ; TISSUE-Kidney;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Kidney; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; McDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Noraalization and subbraction of cap-trapper-selected cDNAs to prepare fiull-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                       MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINS—CS 7BL/64); TISSUB=Kidney;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Natsumai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahiwaji K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik lintegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%; Score 45; DB 2; Length 599; ilarity 77.8%; Pred. No. 1.1e+02; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                   SEQUENCE FROM N.A.
STRARM-EGSPBL/60; TISSUE=Kidney;
MEDILINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 protein.
599 AA; 68022 MW; 4332A8427D33B8DA CRC64;
                                                    Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MGD; MG1:1289164; D15Ertd785e.
InterPro; IPR009378; DUF1032.
Pfam; PF06278; DUF1032; 1.
Hypothetical protein.
SEQUENCE 599 AA; 68022 MW; 4
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Best Local Similarity
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        Carrain-NoD; Tissub=Thymus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Rukuda S., Furnon M., Hanagaki T., Hara A., Hashlame W.,
Rukuda S., Furnon M., Hanagaki T., Haracka T., Hirozane T.,
Ruthara K., Hayatsu W., Hirancto K., Hiracka T., Hirozane T.,
Arch H., Kawai J., Kojima Y., Kondo B., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Salto R., Saltoh H., Sakai C., Sakazume N., Sano H.,
Basaki D., Saltoh H., Sakai C., Sakazume N., Sano H.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yawanishi A., Muramatsu M., Hayashizaki Y.,
Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.
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0
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SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
MEDLINE-2049374; PubMed-11042159; DOI=10.1101/gr.145100;
MEDLINE-20499374. PubMed-11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAIN=NOD; TISSUB=Thymus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate kidney CDNA, RIKEN full-length enriched
library, clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Wouse),
Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1 protein.
599 AA; 68023 MW; 4332A8427EDA9AB8 CRC64;
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InterPro; IPR009378; DUF1032.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF06278; DUF1032; 1.
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les 7; Conservative
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Search completed: April 12, 2005, 08:05:44 Job time : 73.1818 secs

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AAB72505 standard; peptide; 11
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Best Local Similarity 100.
Matches 11; Conservative
Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                Colostrinin peptide #6
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AAB72505;
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Aab72251 Colostrin
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## ALIGNMENTS

Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient Length 11; Dermatological; oxidative stress regulator; colostrinin. Boldogh I; Ź Claim 6; Page 25; 48pp; English

Gape ö Indels 100.0%; Score 62; DB 4; I 100.0%; Pred. No. 0.00033; ive 0; Mismatches 0;

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RESULT AAB593

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Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin, a proline rich polypeptide aggregate contained in colostrum. The peptides have immune response modulatory activity, and are capable of inducting cytokines. Colostrinin and its derived peptides are useful for inducing cytokine production, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders, mental disorders, dementia, neurodegenerative diseases, Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic disorders of the immune system, bacterial and viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective; neural cell differentiation regulator; colostrinin;
dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                                                                                                                                                                                                                                                                                Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 4; Length 11; 100.0%; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                Boldogh I, Georgiades J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquired immunological deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB72537 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                                                                            (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2000; 2000WO-US022774.
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                                                                                                                                                                   .7-AUG-2000; 2000WO-US022818.
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                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM.
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                       neurosis; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
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                                                                                                WO200111937-A2
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                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized
                                                                                                                                                                                                                                                                                   Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 4; L
100.0%; Pred. No. 0.00033;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                  colostrinin peptide fragment A-2.
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                                                                                                                                        AABS9311 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-00012852.
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                                                                                                                                                                                                               (first entry)
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                          MPQNFYKLPOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                               WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1999;
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                                                                                                                                                                               AAB59311;
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Best Loc Matches

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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. Methods are claimed for: inducing a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell by contact with an immunological regulator. Corganism, and the cell is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions effective to induce a cytokine; modulating an immune response in a patient by administering an immunological regulator under conditions effective to induce a cytokine, where the immune response is specific or non specific, an interferon regulator is administered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cells with a blood cell regulator, where the blood cells are increased in number or differentiated; and a method for modulating blood cell proliferation in a patent. A claimed method for modulating blood cell proliferation in a patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
                                                                                                                                                               5; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colostrinin; colostrum; immunomodulator; cardiovascular;
blood cell regulator; cytokine inducer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optional C-terminal amidation"
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                                                                                                                                                            100.0%; Score 62; DB 5; I 100.0%; Pred. No. 0.00033;
                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAM51041 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colostrinin constituent peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 34; 54pp; English.
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(REGE-) REGEN THERAPEUTICS PLC.
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                                                                                                                                                                                                                                                                               Hughes TK,
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                                                                                                                                                            Query Match
Best Local Similarity
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Modified-site
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Matches
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                                                                                                                                       Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                                                                                                                                                          The present invention relates to a method for promoting neural cell afferentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell differentiation; neural cell regulator; colostrinin peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoting cell differentiation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
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100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                Claim 6; Page 21; 35pp; English.
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                                                                                               WPI; 2001-226545/23.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
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AA014582;

RESULT 5 AAO14582

8 8 Neural neural

analog

research. The present

transplantation, implantation, or scientific sequence is a colostrinin constituent peptide

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Gaps

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11; Conservative

Matches

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Query Match Best Local Similarity

Sequence 11 AA;

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Length 11; Indels

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The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, organ, or organism, or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/ after a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of in the cell, such as decreases or prevents increase in the level of in the cell, such as decreases or prevents increase in the level of clause to the same conditions when the oxidative stress results in regulator is not present. The modulation of oxidative stress results in enhanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skiin, and the other internal and external organs), as well as enhanced preservation of such organs for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
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cytokine-inducing composition comprises a pharmaceutical carrier and active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colostrinin constituent peptide #6
                                                                                                                                                                                                                                                                                                                                                                                  AAE20233 standard; peptide; 11 AA.
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                                                                                                                                                                          Similarity
                                                                                                               Sequence 11 AA;
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Modified-site
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Best Local 9
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The present invention describes the use of a modulator selected from colostrinin, its constituent peptide, its active analogue, and a colostrinin, its constituent peptide, its active analogue, and a colostrinin, its constituent peptide, its active analogue, and a colostrinin and required lipid peroxidation in a cell, in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, protecting against DNA damage in a cell.

The modulator has cytostatic activity, and can be used as a 4HNE coloring thms. The modulator is useful in the manufacture of a medicament for reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated colorining 4HNE-induced activation of p53 protein, colostrinin, or its constituent peptide or active analogue is useful for inhibiting apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of colostrinin for e.g. modulating an intracellular signaling molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in a cell.
                                                                                                                                                                                                                      modulator; colostrinin; intracellular signaling molecule modulator; 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor; 4HNE-protein adduct firmation reduction; 4HNE-mediated glutathione deplation inhibition; p53 inhibition; c-Jun NH2-terminal Kinase inhibition.
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                                                                                                                                                                                             Constituent peptide of colostrinin SEQ ID NO:6.
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                                                                                          ADN60300 standard; peptide; 11 AA.
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STANTON J G.
GEORGIADES J A.
HUGHES T K.
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1 MPQNFYKLPOM 11
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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(GEOR/)
(HUGH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a peptide that can be recovered from covine colostrinin using the method of the invention. The invention of provides a method for the recovery of peptides (especially colostrinin) from colostrum in substantially pure, biologically active form and in high yield. The method involves mixing the colostrum with an alcohol to form an alcohol phase containing the colostrinin and a precipitate containing higher molecular weight caseins and other proteins. Best results are obtained using methanol or ethanol of at least 80%, and preferably up to 100%, purity. The alcohol phase is then separated from the precipitate, and the colostrinin is separated from the alcohol, preferably by evaporation, to form a colostrinin-rich phase, which is recovered. A precipitation agent, such as ammonium sulfate, may be added to induce precipitation of the colostrinin peptides. The method is generally applicable to the separation of peptides from fluids containing and a molecular weight proteins, lipids, carbohydrates and/or nucleic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recovering peptides such as colostrinin from mammalian colostrum, by mixing colostrum with alcohol to form alcohol phase containing peptides and precipitate, separating alcohol phase from precipitate, and recovering alcohol phase.
The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
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100.0%; Pred. No. 0.00033;
ive 0; Mismatches 0;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                   ADS74387 standard; peptide; 11 AA.
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08-MAR-2004; 2004GB-00005190.
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                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                     Ovine colostrinin peptide
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Matches 11; Conservative
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                                                 Sequence 11 AA;
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Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptid fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and promote the dissolution of beta-amyloid plaques
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                                                                                                                                                                                                                                                                                                                                                                                      colostrinin peptide fragment derived sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome derived single exon protein #4858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABOS8624 standard; protein; 164 AA.
                                                                                                                                                                                                         AAB59342 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32-JUN-2000; 2000WO-GB002128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-00012852
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
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MPONFYKLPOM 11
                                  MPQNFYKLPQM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                 21-MAR-2001
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ADM04386 standard; protein; 511 AA

ADM04386

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide agraces in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any. of the 6888 amino acids equences concolding at least 8 amino acids of any. of the 6888 amino acids equences of the properties of any of the 6888 amino acids mino acids of stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid plurality of probes for measuring human gene expression, a method of a datessably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of configuous amino acids of any of the above-mentioned amino acids of solling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression date by subscription, and a computer-readable corporated above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying the above. The probe, methods and apparatus are useful in gene capression analysis. The probes are used in identifying and characterising gross and lerrative splicing events, in priming the synthesis of nucleic acids, or in expressing the Orbe protein of the inventor in priming the synthesis of nucleic acids, or in expressing the Orbe protein of the propes of this patent did not format directly from USPTO at this patent did not format directly from USPTO a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.5%; Score 40; DB 8; Length 164; 60.0%; Pred. No. 42; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20030194704
alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 45; SEQ ID NO 32258; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Penn SG, Rank DR, Hanzel DK;
                                                                                                                                                                                  3-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                             03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-119264/12
                                                                                                                                                                                                                                                                      (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 164 AA;
                                                                                          US2003194704-A1.
                                               Homo sapiens
                                                                                                                                     16-0CT-2003.
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention ApM65202-ApM66731 is useful therapy. An oligonucleotide of the invention ApM66202-ApM66731 is useful detecting the polynucleotide. The polynucleotide or as a probe for useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone, growth hormone 74.03; cardiovascular disease; development disorder; pregnancy relative disease; tumour; immunological disease; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.5%; Score 40; DB 7; Length 511; 60.0%; Pred. No. 1.3e+02; ive 3; Mismatches 1; Indels
                                                                                                  human; gene therapy; diagnostic marker; pharmaceutical.
                                                                    Human protein of the invention SEQ ID NO:3071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 3071; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP71874 standard; protein; 673 AA.
                                                                                                                                                                                                                                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                             12-APR-2002; 2002EP-00008400.
                                                                                                                                                                                                                                                      22-MAR-2002; 2002JP-00137785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 LPKSFYKAPQ 210
                                                                                                                                                                                                                                                                                                                   Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPQNFYKLPQ 10
                                                                                                                                                                                                                                                                                                                                   Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth hormone 74.03.
                                                                                                                                                                                                                                                                                                                                                                               2003-723558/69.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADM01943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 511 AA;
                                                                                                                                     Homo sapiens.
                                                                                                                                                                EP1347046-A1.
                                          20-MAY-2004
                                                                                                                                                                                                                                                                                                                    Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP71874;
              ADM04386;
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Matches
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Gaps ö

> 6; Conservative 1 MPONFYKLPQ 10 37 LPKSFYKAPO 46

Local Similarity

Best Loc Matches

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reaction (PCR) primers, oligomers, and for chromosome and gene (11) reaction (PCR) primers, oligomers, and for chromosome and gene (11) reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this
                                                                                                                                                                           invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; antionaemic, anticoagulant; thrombolytic; vulnerary; antillex; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q22.1-22.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang J, Wehrman T;
                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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60.0%; Pred. No. 1.8e+02;
iive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel polypeptide sequence, SEQ ID NO:1761.
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                                                                                                                               Claim 20; SEQ ID NO 54409; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang J, Ren F, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC31679 standard; protein; 716 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2002; 2002WO-US030474.
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406 LPKSFYKAPQ 415
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 716 AA
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                                                                                        biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pregnancy relative disease, various tumours, immunological diseases and some inflammations. The invention also discloses the antagonist resisting the polypeptide and its treatment effect, and the application of the polymucleotide. The present sequence represents the growth hormone 74.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the novel polypeptide, growth hormone 74.03, and the polynucleotide encoding it. The polypeptide is useful in treating various diseases, such as cardiovascular diseases, development disorder,
                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide-growth hormone 74.03 and polynucleotide for encoding such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27-28 (Disclosure); 34pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 6; 1
Pred. No. 1.7e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                            (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #24041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG24050 standard; protein; 716 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.5%;
                                                                                                                                                    10-JAN-2001; 2001CN-00105152
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23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                10-JAN-2001; 2001CN-00105152
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Best Local Similarity 60.0%,
Best Local 6, Conservative
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353 LPKSFYKAPQ 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 673 AA;
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                                                                                                                                                                                                                                                                                        Xie Y;
                    Unidentified
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                                                              CN1364813-A.
                                                                                                          21-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide.
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ABG24050;

RESULT 14 ABG24050

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Weng G;
 Wang Z,
 Ma Y, Asundi V,
 Zhou P, Ghosh M, Wang D, M:
Haley-Vicente D, Drmanac RT;
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WPI; 2003-371981/35. N-PSDB; ADC30708 New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer.

Claim 20; SEQ ID NO 1761; 1185pp; English

The invention relates to 971 movel human cDNA sequences (ADC29919-CC ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the vectors and host cells comprising a mucleic acid of the invention; he recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody companies a polypeptide of the invention; and methods of invention further discloses methods for the invention; and methods of compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The complicating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the envention or complication; methods for the identification of compounds that modulate the invention are activity of the polymucleotide and/or polypeptide; and 767 conting sequences corresponding to the cDNA sequences of the invention are expression or activity of the polymucleotide and/or polypeptide; and 767 conting sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the captual products dependent on DNA and amino acid sequences. They are companied diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as phyridisation probes or cancer. The nucleic acids may also be used as phyridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and an anaement of the present sequence represents a specifically. claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. 

Sequence 716 AA;

Gaps ö 64.5%; Score 40; DB 7; Length 716; 60.0%; Pred. No. 1.88+02; tive 3; Mismatches 1; Indels Query Match 64.5 Best Local Similarity 60.0 Matches 6; Conservative

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1 MPQNFYKLPQ 10

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Search completed: April 12, 2005, 08:18:23 Job time : 63.6 secs

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US-09-641-803-6
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Sequence 24603, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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9282, Ap
4282, Ap
22239, A
4, Appli
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2, Appli
15493, A
35851, A
51068, A
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Appli
                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          April 12, 2005, 07:49:30 ; Search time 12.9 Seconds (without alignments) 63.654 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2
Sequence 2
Sequence 2
Sequence 1
Sequence 3
Sequence 3
Sequence 5
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Sequence 5
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Sequence 4
Sequence 5
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1: /cgn2_6/ptodatea1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatea1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatea1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodatea1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodatea1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodatea1/iaa/PCTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-641-803-6
US-09-248-796A-24603
US-09-248-776-2
US-09-227-804-2
US-09-334-220-1
US-09-334-220-1
US-09-334-220-1
US-09-348-220-2
US-09-270-767-51068
US-09-270-767-51068
US-09-270-767-51068
US-09-270-767-51068
US-09-270-767-51068
US-09-318-352-4282
US-09-318-352-4282
US-09-318-352-4282
US-09-318-35-4
US-08-486-196-4
US-08-486-196-4
US-08-486-196-4
US-08-486-196-4
US-08-134-000C-5667
US-08-252-991A-23023
US-08-66-645A-7
US-08-60-645A-7
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-955-041-4
                                                                                                                                                                 513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                  1 MPQNFYKLPQM 11
                                                                                                US-10-691-330-6
62
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                      Database
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US-09-248-796A-24603
US-09-248-796A-24603
US-09-248-796A-24603
Sequence 24603, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,132
FILE REFERENCE: 107199-02-12
PRIOR APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1999-08-13
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US-09-641-803-6

Sequence 6, Application US/09641803

Sequence 6, Application US/09641803

Sequence 6, Application US/09641803

Setent No. 6500798

GENERAL INFORMATION:

APPLICANT: STANTON, G. John

TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

FILE REPERROCE: 265.00220101

CURRENT PILING DATE: 2000-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

SOFTWARRE: PALENTIN NUMBER: 60/149,310

PRIOR FILING DATE: 200-08-17

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 6

LENGTH: 11

TADE: DEPTITE THE TENT OF THE TENT OF
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2, Appli
20, Appl
43731, A
14, Appl
3888, Ap
9438, Ap
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Sequence 3 Sequence 3 Sequence 3 Sequence 1 Sequence 1 Sequence 2 Sequence 5 Sequence 5 Sequence 2 Sequence 3 
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                                                                                                                                   US-09-645-192-13
US-10-084-406-13
US-09-031-385-151
US-09-257-179-64
US-09-589-7330-2
US-09-589-733C-2
US-09-589-733C-2
US-09-589-733C-2
US-09-52-188-14
US-09-625-188-14
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US-09-583-110-5097
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US-08-481-190-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                        1 MPQNFYKLPQM 11
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Gaps
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       Sequence 2, Application US/09224772

Sequence 2, Application US/09224772

Patent No. 6207162

GENERAL INFORMATION:
APPLICANT: Reichard, Names R.
TITLE OF INVENTION: NOVEL aspS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEB: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville
STARE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reichard, Raymond W.
APPLICANT: Brown, James R.
APPLICANT: Lawlor, Elizabeth J.
IITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STREET: NJ
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 3 Pred. No. 42; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REPERENCE/DOCKET NUMBER: GM10049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/899,244
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-227-804-2; Sequence 2, Application US/09227804; Patent No. 6265188
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 08543
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 PGNFYALPO 198
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US-09-224-772-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                  ) LOCATION: (12)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-248-796A-24603
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                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                           Score 40; DB 4; Length 66;
Pred. No. 2.9;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-899-244-2
; Sequence 2, Application US/08899244
; Patent No. 5882892
; GENERAL INFORMATION:
APPLICANT: Resichard, Raymond W.
APPLICANT: Brown, James R.
TITLE OF INVENTION: NOVEL aspS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 0843
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CUSTWARE: FastSED for Windows Version 2.0
CUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REFERENCE/DOCKET NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                             64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 24603
LENGTH: 66
                                                                         ORGANISM: Candida albicans
                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 609-520-3259
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                    1 MPQNFYKLPQ 10
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US-08-899-244-2
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Best Local Similarity
Matches 7; Conserv
                                                                                                                NAME/KEY: UNSURE
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TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
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Best Local Similarity 66...
6; Conservative
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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1236 LPQNFYEKP 1244
                                                                                                                                                                                                                                         , ORGANISM: Mus musculus US-09-334-220-2
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82 PQNFFLLPE 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: St. Judes Children's Research Hospital
APPLICANT: Curran, Touran, Touran, Touran, Touran, Touran, Trills OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND
TITLE OF INVENTION: THERAPIES
FILE REFERENCE: 2427/0F704
CURRENT APPLICATION NUMBER: US/09/334,220
CURRENT APPLICATION NUMBER: US/09/334,220
CURRENT FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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66.7%; Pred. No. 2.7e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 582; 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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; Sequence 2, Application US/09334220
; Patent No. 6323177
; GENERAL INFORMATION;
; APPLICANT: St. Judes Children's Research Hospital
             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASICED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,804
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
Pred. No. 4
                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/899,244
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: 8100m, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 29,135
TELEPHONE: 609-520-3214
TELEPAX: 609-520-3214
                                                                                                                                                                                                                                                           GM10049
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Patent No. 6323177
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 582 amino acids TYPE: amino acid STRANDEDNESS: single : TOPOLOGY: linear US-09-227-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Diskette
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1235 LPQNFYEKP 1243
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US-09-334-220-1
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Best Local Similarity
Matches 6; Conserv
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US-09-248-796A-15493
Sequence 15493, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WOMBER: US/09/248,796A
TITLE OF INVENTION: WOMBER: US/09/248,796A
TITLE OF INVENTION WOMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/09/4,725
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US/09/6,409
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 28208
SEQ ID NO 15493
APPLICANT: Curran, Thomas

Applicant: D'Arcangelo, Gabriella
TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
TITLE OF INVENTION: THERAPIES
TITLE OF INVENTION: THERAPIES
FILE REPERBRENCE: 2427/097704.
CURRENT FILING DATE: 1999-06-16
VURBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 3461
TYPE: PRT
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 35851

LENGTH: 411
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Pred. No. 34;
2; Mismatches 1; Indels
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66.7%; Pred. No. 2.7e+02;
iive 2; Mismatches 1
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Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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386 MPNNFSEMPQ 395
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Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-328-352-4282
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US-09-270-767-51068
is Sequence 51068, Application US/09270767
is Sequence 51068, Application US/09270767
j Patent No. 6703491
j Patent No. 6703491
j Patent No. 6703491
j TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT PAPLICATION NUMBER: US/09/270, 767
j CURRENT PILING DATE: 1999-03-17
j NUMBER OF SEQ ID NOS: 62517
j SEQ ID NO 51068
j EBNGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: US/09/27,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurabatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Length 411;
                                                             Length 411;
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                                                                                                1; Indels
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                                                               Score 37; DB 4;
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Xaa means any amino acid US-09-270-767-51068
           ; OTHER INFORMATION: Xea means any amino acid US-09-270-767-35851
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Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.78;
                                                                  59.7%;
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                    Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                         167 MPONFOKL 174
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US-09-538-092-999
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1 MPQNFYKLPQ 10

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Sequence 22239, Application US/09248796A
Sequence 22239, Application US/09248796A
Sequence 22239, Application US/09248796A
GENERAL INFORMATION:
SAPULICANT: Rélath Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4282. Application US/09328352

Sequence 4282. Application US/09328352

Patent No. 652958

Patent No. 652958

Patent No. 652958

APPLICANT GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4282

SEQ ID NO 4282
Sequence 9282, Application US/09949016
; Sequence 9282, Application US/09949016
; Ratent No. 6812339
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WICH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WINDER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PILING DATE: 2000-10-20
; PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-00-03
; PRIOR FILING DATE: 2000-00-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NO 9282
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US-09-328-352-4282
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Search completed: April 12, 2005, 08:07:53 Job time : 13.9 secs

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Sequence 4, Application US/08118906
; Sequence 4, Application US/08118906
; Patent No. 5484590
; GENERAL INFORMATION:
    APPLICANT: Blachnizaen, Marti F.A.
; APPLICANT: Blachnizaen, Marti F.A.
; TITLE OF INVENTION: Antigen By a Cloned Human cDNA Encoding a Member of a TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase Gene Family NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Campbell and Flores
; STRET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.1%; Score 36; DB 4; Length 89; Best Local Similarity 66.7%; Pred. No. 21; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/08/118,906

FILING DATE: 09-58P-1993

ATTORNEY/AGENT INFORMATION:

NAME: CAMPATION NUMBER: P-LJ 9526

TELEPRATION NUMBER: P-LJ 9526

TELEPRATION NUMBER: P-LJ 9526

TELEPRATION NUMBER: P-LJ 9526

TELEPRATION INFORMATION:

TELEPRATION OF SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acide

TYPE: amino acide

TYPE: amino acide

TYPE: Amino acide
                      CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION UNMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22239
LENGTH: 89
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
REFERENCE: 107196.132
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MOLECULE TYPE: protein

US-08-118-906-4
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56 IPSNFYKEP 64
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Best Local Similarity
Matches 6; Conserv
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Sequence 6, Appli
Sequence 3228, A
Sequence 3071, Ap
Sequence 5216, A
Sequence 65516, A
Sequence 1624, Ap
Sequence 46, Appl
Sequence 250800,
Sequence 250800,
Sequence 15737, A
Sequence 15733, Sequence 150738,
                                                                                                                             April 12, 2005, 07:49:30 ; Search time 34.1 Seconds (without alignments) 107.096 Million cell updates/sec
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1: /cgm2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgm2_6/ptodata/1/pubpaa/PCT MEW_PUB.pep:*
2: /cgm2_6/ptodata/1/pubpaa/NCT MEW_PUB.pep:*
4: /cgm2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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11: /cgm2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgm2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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19: /cgm2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                               1 MPQNFYKLPQM 11
                                                                                                                                                                                                               US-10-691-330-6
62
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Match Length DB
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                                                                                      OM protein
                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                  Run on:
                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
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Sequence 216, App Sequence 19918, A Sequence 19918, A Sequence 1991, A Sequence 5, Appli Sequence 13, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1199, App Sequence 1151, Appli Sequence 151, Appli Sequence 151, Appli Sequence 64, Appli Sequence 64, Appli Sequence 1915, Appli Sequence 1151, Appli Sequence 2, Appli 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Appli
Sequence 20, Appl
15 US-10-424-599-188125
15 US-10-082-830-236
15 US-10-424-599-189125
15 US-10-424-599-199428
16 US-10-767-701-5423
16 US-10-767-701-5423
18 US-10-767-701-5423
19 US-09-547-267-7
10 US-09-547-267-7
11 US-10-982-980-5
12 US-10-984-980-5
13 US-10-984-98-198
13 US-10-087-192-1998
13 US-10-087-192-1998
13 US-10-087-192-1998
13 US-10-087-192-1998
13 US-10-087-192-1998
14 US-10-372-6639-151
15 US-10-363-144453
15 US-10-363-324-1045
15 US-10-363-324-106
16 US-10-363-324-108
17 US-10-363-324-108
18 US-10-363-324-108
19 US-09-729-835-64
15 US-10-363-324-108
16 US-10-363-324-108
17 US-10-363-324-108
18 US-10-424-599-19896
19 US-09-729-198-151
19 US-10-424-599-19896
                                                                                                                                                                                                                                                                                                   1038
11349
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### ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: STATEORY

TITLE OF INVENTION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: peptide US-10-281-652-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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Best Local S
Matches 11
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1 MPQNFYKLPQM 11

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                                                                                                                                                          sequence 3071, Application US/10108260A; Bublication No. US20040005560A1; Bublication No. US20040005560A1; GENERAL INFORMATION:
APPLICANT: HELLIX RESEARCH INSTITUTE; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27, NUMBER OF SEQ ID NOS: 5458; SOFTWARE; Patentin Ver. 2.1; SEQ ID NO 3011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
64.5%; Score 40; DB 17; Length 878;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 15;
Pred. No. 1.2e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE KEFKERM APPLICATION NUMBER: US/10/825,692
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/329,533
PRIOR FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-10-17
PRIOR PLICATION NUMBER: US 60/332,007
PRIOR PLICATION NUMBER: US 60/375,404
PRIOR PLICATION NUMBER: US 60/375,404
PRIOR PLILNG DATE: 2002-04-26
PRIOR PLILNG DATE: 2002-04-26
PRIOR PLILNG DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATCHIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Botazzi, Maria E.
APPLICANT: Mendez, Susana
TITLE OF INVENTION: Hookworm Vaccine
FILE REFERENCE: 03740007aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 92, Application US/10825692
Publication No. US20050042232A1
GENERAL INFORMATION:
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Loukas, Alexander
Williamson, Angela
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US-10-825-692-92
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Bdamchian, Mahnaz
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Goud, Gaddam
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Matches 6; Conservative
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37 LPKSFYKAPQ 46
1 MPONFYKLPQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3071
                                                                                                                                  RESULT 4
US-10-108-260A-3071
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SEQ ID NO 92
LENGTH: 878
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US-10-029-386-32258, Application US/10029386

| Sequence 32258, Application No. US20030194704A1
| Seducine 32258, Application No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Hanzel, David K. TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION: EXPRESSION ANALYSIS TWO TITLE OF INVENTION: USAPEL NOT TO NOTHING DATE: 2001-12-20
| CURRENT FILING DATE: 2001-12-20
| NUMBER OF SEQ ID NOS: 34288
| SEQ ID NO 32258 Annomax Sequence Listing Engine vers. 1.1
| SEQ ID NO 32258
                                                                                                                                                          APPLICANT: Stanton, G. John
APPLICANT: Stanton, G. John
APPLICANT: Stanton, G. John
APPLICANT: Stanton, G. John
APPLICANT: Georgiades, Jerzy A.
APPLICANT: Georgiades, Thomas K., Jr.
APPLICANT: Hughes, Thomas K., Jr.
APPLICANT: Kruzel, Marian
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
TITLE OF INVENTION: THEREOF AS INHIBITORS OF APOPTOSIS AND OTHER CELLULAR DAMAGE
FILE REFERRACE: 265.00390101
CURRENT PELING DATE: 2003-10-22
PRIOR PILING DATE: 2003-10-22
PRIOR PLING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 17; Length 11; Local Similarity 100.0%; Pred. No. 0.00031; 108 11; Conservative 0; Mismathland
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CTHER INFORMATION: EXPRESSED IN PELACENTA, SIGNAL = 2.1
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
CTHER INFORMATION: SYPRESSED IN BONE MARROW, SIGNAL = 1.5
CTHER INFORMATION: SYRESSED IN BONE MARROW, SIGNAL = 1.5
CTHER INFORMATION: SWISSPROT HIT: Q01656, EVALUE 5.00e-21
US-10-029-386-32258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
, OTHER INFORMATION: Synthetic Peptides
US-10-691-330-6
                                                                                  Sequence 6, Application US/10691330 Publication No. US20050042300A1 GENERAL INFORMATION:
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1 MPQNFYKLPQM 11
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
LENGTH: 11
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SEQ ID NO 1624
LENGTH: 3427
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELLTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-66
FRIOR FILING DATE: 2000-05-66
FRIOR FILING DATE: 2000-09-06
FRIOR PRIOR POLICATION NUMBER: 60/230,337
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-110-23
FRIOR FILING DATE: 2000-110-23
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2001-02-66
FRIOR FILING DATE: 2001-02-66
FRIOR FILING DATE: 2001-02-66
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-66
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-66
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-66
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
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FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB Pred. No. 2.1e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60569, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                       Sequence 55316, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-282-122A-55316
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.9
Best Local Similarity 77.8
Matches 7; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                             302 MPREFYVLPQ 311
1 MPONFYKLPQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 PGNFYALPO 198
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APPLICANT: Trawnick, John
APPLICANT: Trawnick, John
APPLICANT: Trawnick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFREENCE: ELITHA, 034A
CURRENT APPLICATION NUMBER: 05/10/28, 122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PRILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-16
PRIOR PLILING DATE: 2001-02-16
PRIOR PRILING DATE: 2001-02-16
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APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glan, Gary M.
APPLICANT: Glan, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 15; Length 591;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels
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Publication No. US20040101874A1
GENERAL INFORMATION
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Zhang, Bing
APPLICANT: Ghosh, Bing
APPLICANT: Ghosh, Steven W.
APPLICANT: Taylor, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT CORGANISM: Listeria monocytogenes US-10-282-122A-60569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.1
SEQ ID NO 60569
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yskind, Judith
all, Daniel
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                      Frawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 PGNFYALPQ 197
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Gaps

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1; Indels

Length 3460;

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Score 39; DB 17;
Pred. No. 1.3e+03;
2; Mismatches 1;
         62.9%;
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ORGANISM: Sorghum bicolor
         Query Match 62.9
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                              :|||||: |
1235 LPONFYEKP 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 PHNYYHLPQ 180
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                                                                                                  1 MPQNFYKLP
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Pred. No. 1.3e+03;
2; Mismatches 1; Indels (
                                                                                   121,
133,
145,
157,
                                                                                 120,
132,
144,
156,
                                                                                   119,
131,
143,
155,
                                                              | NAME/KEY: VARIANT
| LOCATION: 113, 114, 115, 116, 117, 1
| LOCATION: 125, 126, 127, 128, 129, 1
| LOCATION: 137, 138, 139, 140, 141, 1
| LOCATION: 149, 150, 151, 152, 153, 1
| COTHER INFORMATION: Xaa = Any Amino of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-753-267-46

; Sequence 46. Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                               62.9%;
                                                                                                                                                                                                                            Query Match
Best Local Similarity 66...
G. Conservative
                                                                                                                                                                                                                                                                                                                                                                                     1235 LPONFYEKP 1243
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ORGANISM: Homo Sapiens
US-10-753-267-46
                     Homo sapiens
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                     ORGANISM:
                                      FEATURE:
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RESULT 10
US-10-424-599-250800
US-10-424-599-250800
Subject on US20040031072A1
Subject on No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 250800
LENGTH: 248
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APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwa

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: DIABLES US 10/10/767,701

CURRENT APPLICATION NUMBER: US 10/10/767,701

CURRENT FILING DATE: 2004-01-29

SEQ ID NOS: 63128

SEQ ID NO 45737

LENGTH: 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
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US-10-767-701-45737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_68501C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.3%; Score 38; DB 15; Le Best Local Similarity 66.7%; Pred. No. 1.3e+02; Matches 6; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(248)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45737, Application US/10767701
; Publication No. US20040172684A1
GENERAL INFORMATION:
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Sequence 188125, Application US/10424599

Sequence 188125, Application US/20403107241

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 188125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAPPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0249
CURRENT APPLICATION NUMBER: US/10/082,830
CURRENT APPLICATION NUMBER: US/243,802
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
SOFTWARE: PATENTIN VOX: 282
SOFTWARE: PATENTIN VOX: 2.1
SEQ ID NO 236
LENGTH: 58
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                                                                                                                                                                 Score 37; DB 11; Length 200;
Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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US-10-424-599-188125
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Pred. No. 60;
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                                                                                                                                                                    59.7%;
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Best Local Similarity 62.5
Lea 5, Conservative
                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                       LENGTH: 200
TYPE: PRT
CRGANISM: Homo sapiens
US-09-801-944B-143
                                                                                                                                                                                                                                                                                                                       177 QNFYSVPQ 184
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38 PKNFWKIP 45
                                                                                                                                                                                                                                                                                   3 QNFYKLPQ 10
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-424-599-188125
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SEQ ID NO 143
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                                                                                         Sequence 150738, Application US/10424599
) Publication vo. US20040031072A1
) GENERAL INFORMATION:
) APPLICANT: La Rosa Thomas J
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 150738
LENGTH: 85
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APPLICANT: Wood, Linda S.

TITLE OF INVENTION: No. US20040014169Alel G Protein-Coupled Receptors
FILE REFERENCE: 00100US;
CURRENT APPLICATION NUMBER: US/09/801,944B

CURRENT PILING DATE: 2003-08-01

PRIOR PELICATION NUMBER: 60/187,828

PRIOR PELICATION NUMBER: 60/187,715

PRIOR PELICATION NUMBER: 60/187,929

PRIOR PELICATION NUMBER: 60/187,929

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%; Score 37.5; DB 15; Length 85; 80.0%; Pred. No. 51; cive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107140C.1.pep
US-10-424-599-150738
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LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-801-944B-143;
Sequence 143, Application US/09801944B
Sequence 143, Application No. US20040014169A1
GENERAL INFORMATION:
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225 PONVYOVPQ 233
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                             RESULT 12
US-10-424-599-150738
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Indels
2;
54.5%; Pred. No. 63; ive 3; Mismatches
Best Local Similarity 54.5%; Matches 6; Conservative
Best Local Matches

0;

1 MPQNFYKLPQM 11 :||:|:|| 28 IPQSFFLLPAM 38

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Search completed: April 12, 2005, 07:55:21 Job time : 34.1 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein April 12, 2005, 07:49:31 ; Search time 7.9 Seconds (without alignments) 133.973 Million cell updates/sec Run on:

US-10-691-330-6 62 1 MPQNFYKLPQM 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	ABC transporter -	aspartyl-tRNA synt	aspartate-tRNA lig	aspartyl-tRNA synt	aspartyl-tRNA synt	reelin precursor -	probable DNA-bindi	hypothetical prote			Balbiani ring a 67	hypothetical prote	UDP-N-acetylmuramo	oligodendrocyte-my	aspartyl-tRNA synt	baseplate protein	hypothetical prote	sex-determining pr	probable aromatic	beta-1,3-galactosy	hypothetical prote	hypothetical prote	hypothetical prote		tyrosine protein k	BNI1 protein - yea	vomeronasal secret	endonuclease precu
SUMMARIES	ID	B72629	H70432	E81660	G71500	AG1264	AI1626	S58870	C96752	F97855	B71642	S62524	JH0365	S75992	F84955	A39613	G87483	G6BPT4	T21021	S26046	C82991	A46293	T23792	T21481	A86145	E87318	T03180	24	18	B70151
	DB		~	7	~	~	7	7	N	7	N	~	~	~	N	~	~	-	~	N	~	~	~	~	~	~	~	7	~	7
	Length	113	247	582	582	591	591	3461	289	445	445	1374	241	566	440	440	609	099	779	184	322	428	478	486	564	909	1186	1953	182	195
	Query Match	66.1	62.9	62.9	62.9	65.9	65.9	65.9	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	59.7	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	56.5	56.5
	Score	41	39	39	39	39	39	39	38	38	38	38	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	35	35
	Result No.		7	3	4	ഗ	v	7	œ	σ	10	11	12	13	14	15	16		18								56			

heat shock protein	conserved hypothet	glycosyltransferas	alpha-D-mannose-al	hypothetical prote	hypothetical prote	cellulose synthase	DNA polymerase III	DNA-directed DNA p	hypothetical prote	verprolin related	hypothetical prote	probable membrane	catechol oxidase (	catechol oxidase (	hypothetical prote
T04316	E83107	AH2858	F97635	T02620	T46219	AF2275	E95103	C97971	T34385	T50949	S46088	S64060	S33540	T07097	AI2652
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210	253	349	363	442	266	693	1042	1042	1070	1072	527	527	296	599	62
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26	26	26	26	56.5	26	26	26	26	56.5	26	55	22	55	55.6	54.8
35	35	32	35	35	35	35	35	35	35	35	34.5	34.5	34.5	34.5	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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hypothetical protein APE1490 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72629 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. G, B3-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72629
A;Status: preliminary
A;Residues: 1-113 <KAW>

A;Cross-references: UNIPROT:09YBW0; DDBJ:AP000061; NID:95104821; PIDN:BAA80488.1; PID:d1 A;Experimental source: strain Kl

A;Gene: APE1490 C;Superfamily: Aeropyrum pernix hypothetical protein APE1490

Gaps ö Length 113; 2; Indels Query Match 66.1%; Score 41; DB 2; Best Local Similarity 54.5%; Pred. No. 1.4; Matches 6; Conservative 3; Mismatches :

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:| ||: ||: LPSNFFSLPRM 25 1 MPQNFYKLPQM 11 15 셤 ò

H70432 ABC transporter - Aquifex aeolicus

C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

Ribeckert, G.; Warren, D.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov C; Accession: H70432

Nature 392, 353-358, 1998 A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300, MUID:98196666, PMID:9537320 A,Accession: H70432

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-247 <AQF> A;Cross-references: UNIPROT:067490; GB:AE000744; NID:g2983891; PIDN:AAC07448.1; PID:g298 A;Experimental source: strain VF5

C;Superfamily: inner membrane protein malK; ATP-binding cassette homology C;Keywords: ATP; nucleotide binding; P-loop F;18-215/Domain: ATP-binding cassette homology <ABC>

8 g

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A;Residues: 1-591 <GLA>
A;Cross-references: UNIPROT:Q92BJ4; GB:AL592022; PIDN:CAC96785.1; PID:g16414041; GSPDB:G
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-591 <GLA>
A;Residues: 1-591 <GLA>
A;Cross-references: UNIPROT:Q8Y709; GB:NC_003210; PIDN:CAC99597.1; PID:g16410948; GSPDB:C.
A;Experimental source: strain EGD-e
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A.; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Maitchors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A.; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                  C;Species: Listeria monocytogenes
C;Decies: Listeria monocytogenes
C;Deceies: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Ad2164
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C;Accession: Ag4-852 2001
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mai
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1264
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C;Species: Mus musculus (house mouse)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;ŝpecies: Listeria innocua
C;bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                       aspartyl-tRNA synthetase [imported] - Listeria monocytogenes (strain EGD-e)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 591;
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19;
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Pred. No.
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C,Superfamily: lysine-tRNA ligase
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77.8%;
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Best Local Similarity 77...
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Best Local Similarity 77.8
Trans 7; Conservative
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A;Molecule type: DNA
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NyAlternate names: aspartyl-tRNA synthetase
C;Species: Chlamydia trachomatis
C;Stecies: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Ju1-2004
C;Stecesion: G71500
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Itile: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, A;Rcession: G71500
A;Reference number: A71570; MUD:99000809; PMID:9784136
A;Accession: G71500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-582 <ARN>
A;Residues: 1-582 <ARN>
A;Residues: 1-582 <ARN>
A;Residues: UNIPROT:084546; GB:AE001325; GB:AE001273; NID:93328980; PIDN:AAC6814
A;Reperimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Genetics:
A;Genetics
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Ciperes 31-Mar-2000 #eequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Ciperes 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Ciperes 31-Mar-2000 #sequence Ciperes 28, 1397-1406, 2000
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Recession: B8166
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-582 < TET>
A;Coss-references: UNIPROT:Q9PJKO; GB:AE002349; GB:AE002160; NID:g7190851; PIDN:AAF3962
C;Genetics: TC0829
C;Superfamily: lysine-tRNA ligase
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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C;Superfamily: lysine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
                                                                                                                                             Gaps
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                                                             Score 39; DB 2; Length 247; pred. No. 7.6; 2; Mismatches 1; Indels
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F;35-42/Region: nucleotide-binding motif A (P-loop
                                                                            62.9%;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                            Query Match 62.9
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity
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A,Status: preliminary
Modecule type: DNA
A,Residues: 1-445 <KUR>
A,Cross-references: UNIPROT: Q92G77; GB:AE006914; PIDN:AAL03784.1; PID:g15620380; GSPDB:G
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A;Cross-references: UNIPROT:009884; EMBL:266569; NID:g1052533; PIDN:CAA91518.1; PID:g105
A;Cross-references: UNIPROT:009884; EmBL:266569; NID:g1052533; PIDN:CAA91518.1; PID:g105
B;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9ZCE8; GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA1523
A;Experimental source: strain Madrid E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: B71642
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 131-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Moseidues: 1-1374 <SEE>
A,Residues: 1-1374 <SEE>
A,Experiments: EMBL:AL032824; PIDN:CAB37423.1; GSPDB:GN00068; SPDB:SPCC584.10c
A,Experimental source: strain 972h-; cosmid c584
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
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C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: T39130; T41432; T41192; S62524
R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Rickettsia prowazekii
C,Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
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Pred. No. 22;
4; Mismatches
                                                                                                                                                                                                                                                                                                                  A;Gene: RC1246
C;Superfamily: conserved hypothetical protein b0835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: conserved hypothetical protein b0835
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Pred. No. 22;
4; Mismatches
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A,Molecule type: DNA
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50.0%;
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50.0%;
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Best Local Similarity 50.0
Matches 5, Conservative
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PQSYYNLPEL 118
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                                                                                       A; Accession: F97855
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                                                                                                                                                                                                                                                                                  C;Genetica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9CA18; GB:AE005173; NID:g6648154; PIDN:AAF21154.1; GSPDB:GN
   C;Accession: SS8870; S71844; I49297
KžD'Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.
Nature 374, 719-723, 1995
A;Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
A;Reference number: I49297; MUID:95231649; PMID:7715726
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C;Species: Rickettsia conorii
C;Dates: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97855
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
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A, Molecule type: mRNA
A, Residues: 1-215, 'T', 217-1905, 'S', 1907-3355,'V', 3357-3391,'N', 3393-3461 < DA2>
A, Cross-references: EMBL:U24703; NID:g902486; PID:g902487
F)-1-27/Domain: signal sequence #status predicted <SIG>
F;28-3461/Product: reelin #status predicted <MAT>
F;1769-1795/Domain: EGF homology <EGF>
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                                                                                                                                                                                               A;Accession: S58870
A;Status: nucleic acid sequence not shown
A;Actaule type: mRNA
A;Residues: 1-3461 cDAR>
A;Crose-references: EMBL:U24703; NID:g902486; PID:g902487
B;D'Arcangelo, G
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Pred. No. 14;
1; Mismatches
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1236 LPQNFYEKP 1244
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186 QNFYKIP 192
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Best Local Similarity
Matches 6; Conserv
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Gaps

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Indels

Length 266;

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Oligodendrocyte-myelin glycoprotein precursor - human C,Species: Homo sapiens (man) C,Species: A36688; A34210; A39613; A310187 R;Mikol, D.D.; Alexakos, M.J.; Bayley, C.A.; Lemons, R.S.; Le Beau, M.M.; Stefansson, K.J.; Mikol, D.D.; Alexakos, M.J.; Bayley, C.A.; Lemons, R.S.; Le Beau, M.M.; Stefansson, K.J.; Lell Structure and chromosomal localization of the gene for the oligodendrocyte-myel; A;Reference number: A36688; MUID:91115958; PMID:2277079
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A; Molecule type: DNA
A; Residues: 1-440 <MIL>
A; Cross-references: UNIPROT: P23515; GB: X57436; NID: G23105; PIDN: CAA40684.1; PID: G23106
A; Cell Biol. 10, 471-479; 1950
J. Cell Biol. 110, 471-479; 1950
A; Title: The oligodendrocyte-myelin glycoprotein belongs to a distinct family of protein
A; Reference number: A34210; MUID: 90130636; PMID: 1688857
A; Accession: A34210.
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A,Residues: 1-20,'X',22-440 <VIS>
A,Residues: 1-20,'X',22-440 <VIS>
A,Rorosa-references: GB:M63623; NID:g189385; PIDN:AAA59970.1; PID:g189386
R,Mikol, D.D.; Stefansson, K.
J. Cell Biol. 106, 1273-1279, 1988
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C;Superfamily: UDP-N-acetylmuramate-alanine ligase
C;Keywords: ligase
                                                                              Score 37; DB 2;
Pred. No. 20;
F;64-71/Region: nucleotide-binding motif A (P-loop)
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Pred. No. 34;
1; Mismatches
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A;Molecule type: DNA
A;Reaidues: 1-440 «STO»
A;Experimental source: strain APS
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Similarity 66.7%;
6; Conservative
                                                                                       Ouery Match 59.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity
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C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
A,Variety: PCC 6803

A,Variety: PCC 6803

C;Accession: S7592

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
C, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75592
A; Accession: S75592
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-266 < KAN>
A; Residues: 1-266 < KAN>
A; Residues: 1-266 < KAN>
A; Cxoss-references: UNIPROT:Q55490; EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA1083
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Note: the nucleotide sequence as submitted to the EMBL Data Library, June 1996
C; Keywords: ATP; nucleotide binding; P-loop
C; Keywords: ATP; nucleotide binding; P-loop
F; 47-242/Domain: ATP-binding cassette homology < ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asiboid ring a 67K protein - midge (Chironomus thummi)
C; Species: Chironomus thummi
C; Species: Chironomus thummi
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C; Accession: Un365
R; Bogachev, S.S.; Blinov, A.G.; Kolesnikov, N.N.; Scherbik, S.V.; Taranin, A.V.; Sebelev Gene 96, 241-247, 1990 for puff (balbiani ring a) in Chironomus thummi may contain a gen A; Title: A tissue-specific puff (balbiani ring a) in Chironomus thummi may contain a gen A; Reference number: UN365
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-21 - 40G>
A; Residues: 1-21 - 40G>
A; Ctoss-references: UNIPROT: P24243; GB:M63152; NID:g156521; PIDN:AAA62726.1; PID:g156522
A; Note: the authors translated the codon GAT for residue 216 as Thr
             submitted to the EMBL Data Library, April 1999
A;Reference number: Z21976
A;Accession: T41192
A;Accession: T41192
A;Acatus: preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:AL049662; PIDN:CAB41233.1; GSPDB:GN00068; SPDB:SPCC188.13c
C;Genetics: cLYEL>
A;Gene: SPAC8A4.08c
C;Genetics: cLYEL>
A;Map postition: 1
C;Genetics: cSEEL>
A;Map postition: 3
F;32-39/Region: nucleotide-binding motif A (P-loop) #status atypical
F;141-146/Region: nucleotide-binding motif B
F;145-148/Region: DEAD/H motif #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 241;
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Pred. No. 18;
2; Mismatches
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75.0%;
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Best Local Similarity 75.0°
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65 KNFFKLPQ 72
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Best Local S
Matches 6
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Gaps

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2; Indels

Length 440;

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A; Title: A phosphatidylinositol-linked peanut agglutinin-binding glycoprotein in central A; Reference number: A30187; MUID:88198371; PMID:3283151
A; Rolecule type: protein
A; Rolecule type: protein
A; Rolecule type: protein
A; Residues: 25-29, 'H', 31, 'H', 33-44, 'D', 46-50, 'P', 52 < MI3>
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: GDB:127563; OMIM:164345
A; Cross-references: GDB:127563; OMIM:164345
A; Torsons: #status abbent
A; Note: this gene lies within an intron of GDB:NFI on the opposite strand
C; Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
C; Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
C; Keywords: blocked carboxyl end; glycoprotein repeat homology < LRR1>
F; 12-74 Domain: signal sequence #status predicted < SIGs
F; 56-78 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR2>
F; 100-123 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 168-191 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 168-191 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 168-191 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 168-191 Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 168-191 Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 216-227 Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 216-227 Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form
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Search completed: April 12, 2005, 07:56:54 Job time : 8.9 secs

1 MPQNFYKLPQ 10 || || ::|| 386 MPNNFSEMPQ 395

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rickettsia rickettsia rickettsia

schizosacch bordetella bradyrhizob synechocyst debaryomyce buchnera ap

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Scoring table:

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MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Craig A., Kyes S., Denten M.S., Nene V., Shallon S.J., Sub B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worferdden G.I., Cummings L.M., Subramanian G.M., Mungall C., Pavis Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
0RFNames=PRT2100w;
Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Barrell B.;
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 465 AA; 53968 MW; 60C4D3CODFD6E260 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.7%; Score 42; DB 2;
63.6%; Pred. No. 32;
ive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00212; UBCc; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
Y808 RICPR
Q7P9Y8
Q92G77
Q68VU1
Q86AH3
DCR1 SCHPO
Q7W5W8
                                                                                                                                                                                                                                                                                                                         MURD_BUCAI
                                                                                                                                                                    Q7WGM0
Q89QF7
Q9VH11
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Q23769
Q6BHZ8
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Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 419:498-511(2002).
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Matches 7; Conservative
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114 IPRNFYCLPQI 124
     1 MPQNFYKLPQM 11
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SEQUENCE FROM N.A.
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     Query Match
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Q81423;
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     SOW KARANA KARAN
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Q7uty6 kndopirell
Q27133 alces alces
Q6C1G0 yarrowia li
Q9nq10 homo sapien
Q9y14 haemonchus
O76751 haemonchus
O67490 quuffex aeo
G9pjko chlamydia m
084546 chlamydia t
P8132 buchnera ap
G6Y88 onion yello
Q92bj4 listeria mo
Q7171 listeria mo
Q9770 listeria mo
Q92qv4 rhizobium m
G6me91 parachlamyd
Q64Km mus musculu
Q8534 mycobacteri
Q8534 mycobacteri
Q8534 gallus gall
Q8534 gallus gall
Q9574 sallus gall
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arabidopsis
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mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8i4z3 plasmodium
                                                                                                                                                                      April 12, 2005, 07:49:31 ; Search time 52.2 Seconds (without alignments) 107.909 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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RELN CHICK
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Q8R8C0
Q9YBW0
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Q8WPD7
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Q9CAI8
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302; Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.; Macomplete sequence of the T. tengcongensis genome."; Genome Res. 12:689-700(2002).

EMBL, AR013156; AAM25260.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.7%; Score 42; DB 2; Length 474; 77.8%; Pred. No. 33; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                         Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
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PIR; B72629; B72629.
Complete proteome; Hypothetical protein.
SEQUENCE 113 AA; 12228 MW; 1945C293782213BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA; 53073 MW; B373A46E9E58B91E CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1490.
OrderedLocusNames=APE1490;
                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                        474 AA
                                                     PRT;
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                   OrderedLocusNames=TTE2087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 2.
Complete proteome.
SEQUENCE 474 AA; 53073
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Best Local Similarity 77.8
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                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MB4;
                                                            QBRBC0
QBRBC0;
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RESULT 2
OGRRG
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                                                                                                                                                                                                                                                                 MEDINE: STRAINE: MEDICAL SECRETARY STRAINE: MEDINE: STRAINE: MEDINE: STRAINE: MEDINE: STRAINE: MEDINE: STRAINE: MEDINE: STRAINE: F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schleener H., Amann R., Reinhardt R.; Complete genome sequence of the marine planctomycete Pirellula spectrain 1."; Paco: Natl. Medical Medical Sci. US.A. 100:8298-8303(2003).
Proc. Natl. Acad. Sci. US.A. 100:8298-8303(2003).
I. CATALYTIC ACTIVITY: ATP + L-aspartate + LRNA(Asp) = AMP + diphosphate + L-aspartate + LRNA(Asp).
I. SUBUNIT: Homodimer (By similarity).
I. SUBCELLULAR LOCATION: Cytoplasmic.
I. SUBCELLULAR LOCATION: Cytoplasmic.
I. SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02938; GAD; 1.
Pfam; PF0152; tRNA-synt_2; 2.
Pfam; PF01336; tRNA-synt_2; 2.
TIGRPAMs; TIGR00459; aspS_bact; 1.
PROSTE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacy1-tRNA_synthetase; ATP-binding; Complete proteome; Ligase;
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                                                                                       (Aspartate--tRNA ligase)
                                                                                                                                             Rhodopirellula baltica.
Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 41; DB 1; Length 592; 77.8%; Pred. No. 64; tive 0; Mismatches 2; Indels
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         05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
ASPARTYL-TRNA synthetase (EC 6.1.1.12) (Aspart (AspRS)
592 AA.
                                                                                                                               Name=aspS; OrderedLocusNames=RB8253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004115; GAD.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR004365; tRNA_anti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00044, -; 1.
InterPro, IPR004524; AspS_bact.
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Best Local Similarity 77...
7, Conservative
   STANDARD;
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Q27939
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Gaps

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1; Indels

Length 262;

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Haemonchus contortus (Barber pole worm).
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida,
Trichostrongyloidea, Haemonchidae; Haemonchinae, Haemonchus.
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         OSONIO:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2010 (TremBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matthews L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132795; CAC00771.1; -.
Interpro; IPR006802; Radial_spoke.
Pfam; PF04712; Radial_spoke; 1.
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SEQUENCE 262 AA; 30374 MW; 424B8386AEA0E084 CRC64;
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Last annotation update)
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60.0%; Pred. No. 80;
iive 3; Mismatches
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                                                    Score 40; DB;
Pred. No. 42;
2; Mismatches
                                                                                                                                                                                                                                                              487 AA.
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                                                      64.5%; Score 40; 66.7%; Pred. No.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity
Matches 6; Conserv
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniauu N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchter C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
Nature 430:35-44(2004).
                                                                                                                                                              MEDLINE=96364219; PubMed=8752004; Gatesy J., Hayashi C., Cronin M.A., Arctander P.; Gatesy J., Hayashi C., Cronin M.A., Arctander P.; Evidence from milk casein genes that cetaceans are close relatives of himomoramid artiodactyls."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to wi|NCU09014.1 Neurospora crassa NCU09014.1 hypothetical
                                     Alces alces (moose).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
Odocoileinae; Alces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG78221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                141 AA; 15763 MW; DC39F68595C13C72 CRC64;
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.5%; Score 40; 70.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                       hippopotamid artiodactyls.";
Mol. Biol. Evol. 13:954-963(1996).
EMBL; U53896; AAB08403.1; -.
                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=YALIOF14421g;
Yarrowia lipolytica CLIB99,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00363; Casein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPQNFYKLPQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|||| |||
22 LPQNFLPLPQ 31
                   B-casein (Fragment
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                           NCBI_TaxID=9852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CLIB99;
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06C100 06C100;

RESULT 6

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Gaps

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Length 487; 1; Indels Length 689;

Gaps

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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RMBL; AY371701; AAQ75756.1; -.
RGO; GO:0016020; C:membrane; IEA.
RGO; GO:004245; F:metallopeptidase activity; IEA.
GO; GO:004245; F:neptallopeptidase activity; IEA.
GO; GO:0004245; F:neptallyein activity; IEA.
GO; GO:0006508; P:proceolyeis and peptidolyeis; IEA.
RICEPPO; IPR007052; NG Mtase.
RICEPPO; IPR000718; Peptidase M13.
RILEPPO; IPR006025; Pept M Zn BS.
RP FFGA9; Peptidase M13.
RP FFGA9; Peptidase M13.
RP ROSITE; PR00092; NG WTASE; UNKNOWN 1.
RPROSITE; PS00042; ZINC PROTEASE; UNKNOWN 1.
RPAGA18e; MASILIOPPOFEASE; UNKNOWN 1.
RPAGA110PTOFEASE; PROTEASE; UNKNOWN 1.
RPGGINCE 902 AA; 101872 MW; 0C9294E77851D25D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392,353-358 (1998).
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL, AE000744, AAC07448.1; -.
BIR; H70432; H70432.
HSSP; P02915; 1BOIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.5%; Score 40; DB 2; I
70.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter.
Name=abcT10; OrderedLocusNames=AQ_1531;
Aquifex aeolicus.
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 MPREFYVLPQ 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPQNFYKLPQ 10
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067490
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                                                                     Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida,
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae, Ancylostoma.
NOSE_TaxID=53326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MOLEGIN;

X MEDLINE=20118043; PubMed=10652118;

MEDLINE=20118043; PubMed=10652118;

A Smith W.D., Smith S.K., Pettit D., Newlands G.F.J., Skuce P.J.;

A Smith W.D., Smith S.K., Pettit D., Newlands G.F.J., Skuce P.J.;

A Smith W.D., Smith S.K., Pettit D., Newlands G.F.J., Skuce P.J.;

A Smith W.D., Smith S.K., Pettit D., Newlands G.F.J., Skuce P.J.;

Fractions from Haemonchus contortus.";

Parasite Immunol. 22:63-71(2000).

R EMBL, AF080172; AAC31568.1; -..

R GO, GO:000237; R:metallopeptidase activity; IEA.

R GO, GO:000237; F:metallopeptidase activity; IEA.

R GO, GO:000237; F:metallopeptidase activity; IEA.

R GO, GO:000237; F:metallopeptidase M.3.

R InterPro; IPR000718; Peptidase M.3.

R InterPro; IPR000719; Prot. Kinase.

R InterPro; IPR000719; Prot. Kinase.

R InterPro; IPR000719; Prot. Kinase.

R Pfam; PF01431; Peptidase M.3. 1.

R Pfam; PF054431; Peptidase M.3. 1.

R Pfam; PF054431; Peptidase M.3. 1.
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 837 AA; 95505 MW; 3681FA41EA66FB3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
putarive zinc metallopeptidase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0786; NEPRILYZIN.
PROSITE, PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
PROSITE; PS00142; ZINC_PRŌTEASE; UNKNOWN 1.
Hydrolase; Metalloprotease; Protease; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             902 AA.
                                                                                                                                                                                                                                                                                                                                                                                         837 AA
                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                Best Local Similarity 70.0%;
Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                373 MPREFYVĽPO 382
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                                                                                                                                           1 MPQNFYKLPQ 10
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RESULT 9
ROT 01-N
DT 01-N
DT
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ö GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000166; F:ATP binding; IEA.
GO; GO:000166; F:ATP binding; IEA.
GO; GO:000166; F:Tanclectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003593; AAA ATPase.
ProDom; PD0000066; ABC_transporter; 1.
ProDom; PD0000066; ABC_transporter; 1. Gaps . 0 62.9%; Score 39; DB 2; Length 247; 66.7%; Pred. No. 60; 1; Indels tive 2; Mismatches 1; Indels PROSITE; PSCS093; ABC_TRANSPORTER_2; 1.
PROSITE; PSCS093; ABC_TRANSPORTER_2; 1.
SEQUENCE 247 AA; 27535 WW; 8C843C4C2F2AFD5F CRC64;

Q6UEA5

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                                                                                                                                                                                                                                                                                                                                       STRAIN=D/UW-J/Cx;
MEDILNES-29008089; Pubmed=9784136; DOI=10.1126/science.282.5389.754;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00338; GAD; 1...
Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF01346; tRNA anti; 1.
TIGRPAMS; TIGRO0459; aspS_bact; 1.
PROSITE; PS50862; AA TRNA_LIGASE II; 1.
Aminoacy1-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 282:754-759(1998).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP + diphosphate + L-asparty1-tRNA(Asp).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-II aminoacy1-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                           Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66227 MW; E8D2EBB2785EFABA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.9%; Score 39; DB 1; I
77.8%; Pred. No. 1.5e+02;
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                                            582 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P36419, 1L0W.
HAMAP; MP 00044; -; 1.
InterPro; IPR00415; GAD.
InterPro; IPR004115; GAD.
InterPro; IPR004115; GAD.
InterPro; IPR004364; RNN-synt 2.
InterPro; IPR002312; RNN-synt 2.
InterPro; IPR002312; RNN-synt anti-
InterPro; IPR004365; RNN-anti-
InterPro; IPR004365; LNN-anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                    Name=aspS; OrderedLocusNames=CT542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001325; AAC68144.1; -. PIR; G71500; G71500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 PGNFYALPO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis
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Best Local Similarity
7, Conserva
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYD_BUCAP
P81432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                              SYD CHL7
                                                                                                                                                                                 (AspRS)
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SYD_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT: 14
                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO04364; ENNA-synt_2.
InterPro; IPRO04364; ENNA-synt_2.
InterPro; IPRO04365; ENNA-synt_asp.
InterPro; IPRO061365; ENNA-anti_
InterPro; IPRO06195; ENNA_ligase_II.
Pfam; PPO0125; ENNA-synt_2; 2.
Pfam; PPO0136; ENNA-synt_1.
PRINTS; PRO1042; FRNASYNTHASP.
TIGREPAM; TGRO0459; aspS bact; 1.
PROSITE; PSS0862; AA TRNA_LIGASE_II; 1.
Aminoacyl-ENNA synthetase; ATP-binding; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae AR39.;
Nucleic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP + diphosphate + L-asparty!-tRNA(Asp).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MIGGS,
MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
White O., Lihher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman Bass S., Lihher K.D., Nelson W.C., DeBoy R.T., Kolonay J.F.,
McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                              16-OCT-2001 (Rel. 40, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
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                                                                                                                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.9%; Score 39; DB 1; Length 582; 77.8%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         582 AA; 66386 MW; 492FC82B8710D420 CRC64;
                                                                                        582 AA
                                                                                                                                                                                                                                                Name=aspS; OrderedLocusNames=TC0829;
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00044; -; 1.
InterPro; IPR004524; AspS_bact.
InterPro; IPR004115; GAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE002349; AAF39629.1; -. PIR; E81660; E81660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 PGNFYALPQ 198
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TIGR; TC0829; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
                                                                                        CHLMU
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HAMAP;

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Gaps

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2; Indels

15-DEC-1998 (Rel. 37, Created)

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Length

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SOW NEW YORK NOT THE PROPERTY OF THE PROPERTY 
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Thao M.L., Baumann P., Bragment from Buchnera aphidicola (Aphid "Nucleotide sequence of a DNA fragment from Buchnera aphidicola (Aphid endosymbiont) containing the genes aspS-trxB-serS-serC-aroA-rpsA-himD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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TIGRRAMs; TIGR00459; aspS_bact; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA_synthetase; ATP-binding; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEQUENCE FROM N.A.
MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
Manuse I., Klasson L., Canbacck B., Naselund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson A.-S.,
"50 million years of genomic stasis in endosymbiotic bacteria.";
$50 million years of genomic stasis in endosymbiotic bacteria.";
-1. CATALYTIC ACTIVITY. ATP + L-aspartate + tRNA(Asp) = AMP +
diphosphate + L-aspartyl-tRNA(Asp).
-1. SUBCELLULAR LOCATOR: Cytoplasmic (By similarity).
-1. SUBCELLULAR LOCATOR: Cytoplasmic (By similarity).
-1. SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
                                                                                                   Name-aspS; OrderedLocusNames=BU8g306;
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacee; Buchnera.
     15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 AA; 67824 MW; F318DFA1654780E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HANAP, MF 00044; 1.

HANAP, MF 00044; 1.

InterPro; IRR004524; AspS bact.

InterPro; IRR0049115; GAD.

InterPro; IRR00494; Nucleic acid OB.

InterPro; IRR004364; tRNA-synt 2.

InterPro; IRR004364; tRNA-synt 2.

InterPro; IRR004365; tRNA-anti.

InterPro; IRR06195; tRNA_ligase_II.

Pfam; PF02938; GAD; 1.

Pfam; PF01336; tRNA-synt 2; 2.

Pfam; PF001336; tRNA_anti.
                                                                                                                                                                                                                                                                                                                                                                                                                Curr. Microbiol. 35:68-69(1997).
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EMBL; AE014107; AAM67860.1; -
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Matches
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586 AA.

PRT;

PRELIMINARY;

RESULT 15 QGYR88 ID QGYR88 AC QGYR88;

2 PQNFYKLPQ 10 | ||| ||| 182 PGNFYALPQ 190

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STRAIN=CY-M;
PubMed=14661021; DOI=10.1038/ng1277;
PubMed=14661021; DOI=10.1038/ng1277;
PubMed=14661021;
PubMed=14661021;
PubMed=14661021;
PubMed=15.,

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GO; GO: 000524; F: Argartate-tRNA ligase activity; IEA.

GO; GO: 0005524; F: RTP binding; IEA.

GO; GO: 0005524; F: RTP binding; IEA.

GO; GO: 0006422; F: argarty1-tRNA aminoacylation; IEA.

InterPro; IPR004524; AspS bact.

InterPro; IPR004364; Nucleic_acid_OB.

InterPro; IPR004364; RNA-synt_2.

InterPro; IPR004365; tRNA-synt_asp.

InterPro; IPR004365; tRNA-synt_asp.

InterPro; IPR006195; tRNA-synt_asp.

InterPro; IPR006195; tRNA-synt_2.

Pfam; PF00123; tRNA-synt_2.
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                                                                                                                                                                                                                                                                                           Onion yellows phytoplasma.
Bacteria, Firmicutes; Mollicutes; Acholeplasmatales;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Acholeplasmataceae; Candidatus Phytoplasma.
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                                                                                                                                                                           Aspartyl-tRNA synthetase.
Name=aspS; OrderedLocusNames=PAM128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00459; aspS_bact; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_1
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Best Local Similarity 77.0.
77. Conservative
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SEQUENCE 586 AA; (
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Stanton GJ, Hughes TK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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 AAB72506;
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 Ewe colos
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                                                                                April 12, 2005, 07:49:31 ; Search time 84 Seconds (without alignments) 69.064 Million cell updates/sec
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Aag19665 P
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Aag38917 P
Aag38917 P
Aae02472 P
Ade37165 E
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Aab72252
Aab7253 G
Aac14583 A
Aam51042 A
Aac2034 G
Ads74388 G
Ads74388 G
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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## ALIGNMENTS

The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinii, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient Modulating oxidative stress level in a cell, involves contacting the with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. Length 15 Dermatological; oxidative stress regulator; colostrinin. Query Match 100.0%; Score 81; DB 4; L Best Local Similarity 100.0%; Pred. No. 9.7e-05; Matches 15; Conservative 0; Mismatches 0; Boldogh I; Ź Claim 6; Page 25; 48pp; English AAB72506 standard; peptide; 15 17-AUG-2000; 2000WO-US022665 99US-0149310P entry) (TEXA ) UNIV TEXAS SYSTEM

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AAB59312;

AAB59312

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sequences AAB72246 - AAB72275 represent peptides derived from clostrinin, a proline rich polypeptide aggregate contained in colostrum. The peptides have immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing production, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological tail disorders, dementia, neurodegenerative diseases, Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic diseases of the immune system, bacterial and viral infections and acquired immunological deficiencies
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dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.
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100.0%; Pred. No. 9.7e-05;
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REGEN THERAPEUTICS PLC
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(REGE-) REGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                               regulator
                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                        Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disease, such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
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100.0%; Pred. No. 9.7e-05;
iive 0; Mismatches 0;
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                                                                                                                                                       AAB59312 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGE-) REGEN THERAPEUTICS PLC
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Matches 15; Conservative
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Length 15; Indels

Boldogh I;

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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell constituent in claimed methods of the invention. Methods are claimed for: inducting a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell by contact with an immunological regulator, corganism, and the cell is mammalian, including human; modulating an corganism, and the cell is mammalian, including human; modulating an corganism conditions effective to induce a cytokine; modulating an immunological regulator under conditions effective to induce a cytokine, where the immunological conditions effective to induce a cytokine, where the immunological regulator under conditions effective to induce a cytokine, where the immune response is specific or non specific, an interferon regulator is administered topically or as part of a dietary supplement. Cand where the immune response; modulating blood cells with a blood cell regulator, where the blood cells or contexting blood cells with a blood cell regulator, where the blood cells are increased in number or differentiated; and a method for modulating blood cell proliferation in a patent. A claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                         Sequence 15 AA;
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                                                                                                                                            Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
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                                                                                                                                                                                                                                                                                    The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB 4; Length 15; Pred. No. 9.7e-05;
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/note= "Optional C-terminal amide"
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100.0%;
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              (TEXA ) UNIV TEXAS SYSTEM
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269152/31.
                                                                                                      WPI; 2001-226545/23
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
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Modified-site
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AA014583;

Query Match

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The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level or each se, or manmalian or human cell present in a cell culture, tissue, or organ, or organism; or for treating oxidative damage to the skin of a premature birth or normal birth, preventing/delaying aging in a premature birth or normal birth, preventing/delaying aging in a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidising species in the cell, such as decreases or prevents increase in the level of an oxidising species in the cell, such as decreases or prevents increase in the level of inpid, compared to the same conditions when the oxidative stress results in regulator is not present. The modulation of oxidative stress results in conditions and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; oxgan; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-4, interleukin-6 and interleukin-10
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                             Length 15;
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                                                                                                                                                                                                                                                                     100.0%; Score 81; DB 5; I
100.0%; Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colostrinin constituent peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE20234 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269151/31.
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                        Sequence 15 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002
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The present invention describes the use of a modulator selected from colostrinin, its constituent peptide, its active analogue, and a colostrinin, its constituent peptide, its active analogue, and a combination of these, for modulating an intracellular signaling molecule in a cell, down regulating 4HRE-mediated lipid peroxidation in a cell, and reducing the toxic effect of beta-amyloid or retinoic acid on a cell. The modulator has cytostatic activity, and can be used as a 4HNE contains a tell in the manufacture of a medicament for inhibitor. The modulator is useful in the manufacture of a medicament for reducing 4HNE-protein adduct formation, inhibiting 4HNE-mediated civation of c-Jun NHZ-terminal kinases and/or inhibiting almost activation of c-Jun NHZ-terminal kinases. Colostrinin, or its constituent peptide or active analogue is useful for inhibiting apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of colostrinin for e.g. modulating an intracellular signaling molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
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                                                                                                                                                                                                                                                                                                                                                                                                  modulator; colostrinin; intracellular signaling molecule modulator; 4HNE-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNE inhibitor; 4HNE-protein adduct formation reduction; 4HNE-mediated glutathione depletion inhibition; p53 inhibition; c-Jun NH2-terminal kinase inhibition.
                                                                                                                     Gaps
transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kruzel M;
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                                                                                                                     0; Indels
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                                                                                       100.0%; Score 81; DB 5; I 100.0%; Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                          Constituent peptide of colostrinin SEQ ID NO:7.
                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                            ADN60301 standard; peptide; 15 AA.
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                                                                                                        Local Similarity 100.
nes 15; Conservative
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STANTON J G.
GEORGIADES J A.
HUGHES T K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanton JG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004037851-A2
                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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(BOLD/)
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(GEOR/)
(HUGH/)
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Matches
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Length 15;

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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georgiades JA;
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                                                                                                                                                                                                                                                                                                         21-MAR-2001
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                                                                                                                                                                                                                                                                     AAB59343;
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                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a peptide that can be recovered from ovine colostrinin using the method of the invention. The invention provides a method for the recovery of peptides (especially colostrinin) from colostrum in substantially pure, biologically active form and in high yield. The method involves mixing the colostrum with an alcohol to form an alcohol phase containing the colostrinin and a precipitate containing higher molecular weight caseins and other proteins. Best results are obtained using methanol or ethanol of at least 80%, and preferably up to 100%, purity. The alcohol phase is then separated from the precipitation dente colostrinin is separated from the alcohol phase or, preferably, to the colostrinin-rich phase. Which is recovered. A precipitation agent, such as ammonium sulfate, may be added either to the alcohol phase or, preferably, to the colostrinin-rich phase to induce precipitation of the colostrinin peptides. The method is generally applicable to the separation of peptides from fluids containing higher molecular weight proteins, lipids, carbohydrates and/or nucleic acids. In an example from the invention, the antigenic profile of peptides recovered from sheep colostrum using the present sequence apprended agained applicable to prepride having the present sequence
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peptides
The present sequence represents a synthetic constituent peptide of colostrinin, which can be used as a modulator in the present invention.
                                                                                                                                    Gaps
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                                                                                            Length 15;
                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colostrum; colostrinin; sheep; peptide purification.
                                                                                            Score 81; DB 8; 1
Pred. No. 9.7e-05;
                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example, SEQ ID NO 3; 41pp; English.
                                                                                                                                                                                                                                                                                                         ADS74388 standard; peptide; 15 AA.
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                                                                                            100.0%;
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08-MAR-2004; 2004GB-00005190.
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                                                                                                                                                                      1 VLEMKFPPPPQETVT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                             Ovine colostrinin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recovering alcohol phase.
                                                                                                              15; Conservative
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                                                          Sequence 15 AA;
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(denoted antigen class A-3).

Sequence 15 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system development of a child's immune system, as a dietary supplement, and to promote the dissolution of beca-amyloid plaques
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Ewe colostrinin peptide fragment derived sequence #3.
                    9.7e-05;
  Score 81; DB 8;
                                                0; Mismatches
                         Pred. No
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                                                                                                                                                                                                                                                                       AAB59343 standard; peptide; 16 AA.
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100.0%;
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AAG38918
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9908-0140693P.
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9908-014138P.
9908-0142842P.
9908-0142842P.
9908-0142862P.
9908-0142862P.
9908-0143842P.
9908-0143842P.
9908-0143842P.
9908-0143842P.
9908-0144086P.
9908-014433P.
9908-014433P.
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03-AUG-1999;
04-AUG-1999;
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06-AUG-1999;
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17-AUG-1999;
18-AUG-1999;
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9905-015303P

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9905-016071P
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69.2%;
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Best Local Similarity 69.2
Matches 9; Conservative
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PR 22-UUC-1999; 999US-0143PP.
PR 22-U
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 23;
1; Mismatches 3; Indels
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121-APR-1999;
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23-APR-1999;
30-APR-1999;
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Pred. No. 25;
1; Mismatches 3; Indels
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 990S-0156596P

990S-015717P

990S-01573E3P

990S-0158232P

990S-0158233P

990S-015929B

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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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69.2%;
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Best Local Similarity
Matches 9; Conserv
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05-MAR-1999;
09-MAR-1999;
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25-MAR-1999;
 29 - SEP - 1999

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0123548P.
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990S-0128714P.
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01-APR-1999;
06-APR-1999;
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3. ARR-1999 0. ARR-1999 0. ARR-1999 0. ARR-1999 6. MAX-1999 6. MAX-1999 7. MAX-1999 4. MAX-1999 4. MAX-1999	19 MAX - 1999; 20 MAX - 1999; 24 MAX - 1999; 25 MAX - 1999; 26 MAX - 1999; 27 MAX - 1999; 28 MAX - 1999; 29 MAX - 1999; 30 - JUN - 1999; 30 - JUN - 1999; 30 - JUN - 1999; 31 - JUN - 1999; 32 - MAX - 1999; 33 - JUN - 1999; 34 - JUN - 1999; 35 - JUN - 1999; 36 - JUN - 1999; 36 - JUN - 1999; 37 - JUN - 1999; 38 - JUN - 1999; 39 - JUN - 1999; 30 - JUN - 1999; 30 - JUN - 1999; 31 - JUN - JUN - 1999; 31 - JUN	2
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Query Match 63.0%; Score 51; DB 3; Length 289; Best Local Similarity 69.2%; Pred. No. 30; Matches 9; Conservative 1; Mismatches 3; Indels
99US-0159634P

99US-0160741P

99US-0160764P

99US-0160768P

99US-016070P

99US-0160815P

99US-0160815P

99US-0160818P

99US-016080P

99US-0160980P

99US-016104P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161920P

99US-0161920P
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Search completed: April 12, 2005, 08:18:25 Job time : 86 secs

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Gaps ö

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Sequence 1, Appli
Sequence 819, App
Sequence 155, App
Sequence 1510, A
Sequence 3, Appli
Sequence 822, Appl
Sequence 20695, A
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Sequence 12610, A
Sequence 9712, Ap
Sequence 1, Appli
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14918, A
9601, Ap
1055, Ap
36510, A
51727, A
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                                                                                                                                         (without alignments)
63.654 Million cell updates/sec
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Sequence 9,
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                                                                                                                      April 12, 2005, 07:49:30 ; Search time 17.5909 Seconds
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Sequence 3
Sequence 8
Sequence 2
Sequence 1
Sequence 1
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Sequence
Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-522-91A-29412
US-09-902-540-12610
US-09-913-227-1
US-08-933-227-1
US-09-538-092-819
US-09-538-092-819
US-09-949-016-11510
US-08-933-227-3
US-09-91A-205-82
US-09-252-91A-20695
US-09-252-91A-20695
US-09-248-796A-14118
US-09-248-796A-14118
US-09-438-1185A-1055
US-09-438-1185A-1055
US-09-318-352-6607
US-09-270-767-36510
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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81
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Match Length DB
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Perfect score:
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                                                                                                                        Run on:
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Sequence 39529, Requence 54746, Sequence 24746, Sequence 37943, Sequence 53160, Sequence 26266, Sequence 14616, Sequence 65, App)
Sequence 745.
Sequence 56,
Sequence 56,
Sequence 316,
Sequence 230
Sequence 230
                                           US-09-211-211-34
US-09-211-021-34
US-09-252-991A-31659
US-09-248-796A-28195
US-09-270-76-39529
US-09-270-76-5446
US-09-270-76-5446
US-09-270-76-7-37943
US-09-270-76-7-53160
US-09-270-76-45380
US-09-270-76-46580
US-09-248-796A-14616
US-09-248-796A-14616
US-09-248-796A-14616
US-09-248-796A-14616
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Sequence 7, Application US/09641803
Sequence 7, Application US/09641803
Fatent No. 6500798
Fatent HUGHES, Thomas K.
FAPLICANT: HUGHES, Thomas K.
FAPLICANT: BOLDOGH, Istvan
FITLE OF INVENTION: US OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND FILE OF INVENTION: US OF COLOSTRININ, CONSTITUENT ESCULATORS
FILE REPERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT PLING DATE: 1099-08-17
FRIOR PLING DATE: 1999-08-17
FRIOR FILING DATE: 1999-08-17
FRIOR PLING DATE: 1999-08-17
FRIOR FILING DATE: 1999-08-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: peptide
US-09-641-803-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEOUL 2.

Sequence 38, Application US/09533029
; Sequence 38, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
    APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Ricchmann, Jose-Luis
; APPLICANT: Ricchmann, Jose-Luis
; APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
; APPLICANT: Samaha, Raymond
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe; Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLEMKPPPPPQETVT 15
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Best Local Similarity 100.
Matches 15; Conservative
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Gaps
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Pred. No. 60;
0; Mismatches 2; Indels
                                                                                                                                    Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-933-227-1
Sequence 1, Application US/08933227
Sequence 1, Application US/08933227
Sequence 1, Application General Sequence 1, APPLICANT: Bandman, Olga
APPLICANT: Guegler, Nail
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOWOLOG
NUMBER OF EGUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYCE Pharmaceuticals, Inc.
                                                                                                                                      DB 4;
45;
                                                                                                                                                                        2; Mismatches
                                                                                                                                         Score 44;
Pred. No. 4
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                                                                                                                                       Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12610
LENGTH: 377
                                                                   TYPE: PRT CRGANISM: Myxococcus xanthus US-09-902-540-12610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                              341 LERHFPPPRQ 351
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                             2 LEMKFPPPPQE 12
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Sequence 29412, Application US/09252991A

Patent No. 651795

Patent No. 651795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANTON: NUCLEIC ACID AND AND AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFRENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PELING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29412
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Bactent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wyxococus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-010

PRIOR APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-010

PRIOR APPLICATION NUMBER: 60/217,883
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                                                                                                                                                                                                                                                                                                                                                DB 4; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
         APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISBASE-INDUCED POLYNUCLEOTIDES
TITLE REPERENCE: MB1-010
CURRENT PILING DATE: 2000-03-22
CURRENT PILING DATE: 1000-03-22
EARLIER PILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 4
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 4
Pred. No. 3.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%;
                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                   63.0%;
69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0.
Local Similarity 80.0.
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                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0
Best Local Similarity 69.2
Matches 9; Conservative
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221 VVEMKFPPDP 230
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                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: G502
US-09-533-029-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-29412
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                                                                                                                                                                                                                                                                                     FEATURE:
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES.

CURRENT APPLICATION NUMBER: 00/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

LENGTH: 498
                                                                APPLICANT: Manafield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-21.
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
RIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatseqFormatter Version 0.9
SEQ ID NO 955
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P18583
US-09-538-092-955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 4; I Pred. No. 1.9e+02;
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Pred. No. 84;
1; Mismatches
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; Sequence 11510, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08933227
Patent No. 5965394
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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698 EKEVPPPKETL 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KFPPPPQETV 14
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-11510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gict. Loic
APPLICANT: Mansfield. Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-54
CURRENT PILING DATE: 2000-03-29
CURRENT FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // NAME/KEY: misc_feature
// LOCATION: (0)...(0)
// OTHER INFORMATION: Polypeptide Accession Number 000505
US-09-538-092-819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                            APPLICATION NUMBER: US/08/933,227 FILING DATE: Filed Herewith PRIOR PAPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-538-092-955
; Sequence 955, Application US/09538092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 819, Application US/09538092 Patent No. 6753314
                                                                                                                                                                               ALTORNET BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF-03
TELEPOMUNICATION INFORMATION:
TELEPHONE: 650-855-055
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STANDEDNESS: single
TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPIPLB01
CLONE: 10403
                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 80.v
Local 8; Conservative
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Matches 8; Conservative
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ORGANISM: Homo sapiens
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Gaps

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2; Indels

Length 1523;

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Gape

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Indels

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Length 498;

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US-09-252-991A-20695

US-09-252-991A-20695

Sequence 20695, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION UNMERS:

1999-02-18

PRIOR FILING DATE:

1998-07-18

PRIOR PRILING DATE:

1998-07-27

NUMBER OF SEQ ID NOS:

33142

LENGTH 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11153, Application US/09902540; Sequence 11153, Application US/09902540; Sequence 11153, Application US/09902540; Patent No. 6833447; Patent No. 6833447; Gregory Linkorkarion: Applicant: Hinkle, Gregory U.; Applicant: Slater, Steven C.; Applicant: Wiegand, Roger C.; Applicant: Wiegand, Roger C.; TITLE OF INVENTION: Waxococcus xanthus Genome Sequences and Uses Thereof; FILLE OF INVENTION: NUMBER: US/09/902,540; CURRENT APPLICATION NUMBER: US/09/902,540; CURRENT FILING DATE: 2001-07-10; PRIOR PPLILING DATE: 2000-07-10; PRIOR FILING DATE: 2000-07-10; NUMBER OF SEQ ID NOS: 16825; SEQ ID NO 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

51.9%; Score 42; DB 4; Length 424;
Best Local Similarity 77.8%; Pred: No. 1e+02;
Matches 7; Conservative 1; Mismatches 1: Indels
                                                                                                                                                                                                         Length 521;
                                                       ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number 000629
US-09-538-092-822
                                                                                                                                                                                                         Score 43; DB 4; Pred. No. 89; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20695
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ORGANISM: Myxococcus xanthus
US-09-902-540-11153
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                           Query Match
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Sequence 822. Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Gict, Loic

APPLICANT: Gict, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE REPERENCE: 1596-542

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 822

LENGTH: 521
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Pred. No. 89;
1; Mismatches 2; Indels
APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
CUNTRX: CA
COUNTRX: USA
ZIP: 943044
COMPUTED PROFER
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
TULNG DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: Filed Herewith
APPLICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PP-0394 US
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
EQUINCE CHARATTERISTICS:
LEAGTH: 521 amino acids
TYPE: amino acids
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
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LIBRARY: GenBank
CLONE: 1928975
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US-09-538-092-822
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366 KLPPPPDÉAV 375

В

NAME/KEY: misc_feature

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RESULT 14
US-09-248-796A-14918

Sequence 14918, Application US/09248796A

Factor No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14918

LENGTH: 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-949-016-9601

i Sequence 9601, Application US/09949016

i Sequence 9601, Application US/09949016

i Batent No. 6812339

i GENERAL INFORMATION:

I TILLE OF INVENTION: FOLYMOKPHISMS IN KNOWN GENES ASSOCIATED

I TILLE OF INVENTION: POLYMOKPHISMS IN KNOWN GENES ASSOCIATED

I TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

I TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

I TILLE OF INVENTION: WITHER (0/241, 755)

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PERESEQ for Windows Version 4.0

SEQ ID NO 9601

LENGTH: 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 4; I Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-14918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-9601
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Search completed: April 12, 2005, 08:07:53 Job time : 17.5909 secs

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Sequence 7, Appli
Sequence 104, Appli
Sequence 104, App
Sequence 314, App
Sequence 314, App
Sequence 38, Appl
Sequence 22, Appl
Sequence 58806, A
Sequence 56806, A
Sequence 188309,
Sequence 188309,
                                                                                                                                         April 12, 2005, 07:49:30 ; Search time 46.5 Seconds (without alignments) 107.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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12. /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.ppp:*

13. /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.ppp:*

14. /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.ppp:*

15. /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.ppp:*

15. /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.ppp:*

16. /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.ppp:*

17. /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.ppp:*

18. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*

19. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*

10. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*

11. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*

12. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

13. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

14. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

15. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

16. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

17. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

18. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*

19. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-10-691-330-7

2 US-10-25-068-104

3 US-10-374-780A-2014

5 US-10-374-780A-2014

7 US-10-495-918-140

7 US-10-495-918-140

8 US-10-286-264-22

4 US-10-286-264-22

4 US-10-278-536-148

5 US-10-493-16890

6 US-10-493-16890

8 US-10-424-599-158909

US-09-864-761-37299
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                                                                                                                                                                                                                                                                                                                                                                                                             1418010 seqs, 331997259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                 81
1 VLEMKFPPPPQETVT 15
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                   Perfect score:
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                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                              Run on:
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Sequence 220767, Sequence 127360, Sequence 170529, Sequence 176514, Sequence 265006,	1614 86, 10, 2810 4062	Sequence 167, App Sequence 33614, A Sequence 34141, A Sequence 166810, Sequence 159499, Sequence 154, App Sequence 866, App	Sequence 196028, Sequence 3352, A Sequence 3267, Sequence 22677, Sequence 175326, Sequence 103502, Sequence 103502,	Sequence 1039, Ap Sequence 35, Appl Sequence 47, Appl Sequence 47, Appl Sequence 1702, Ap Sequence 181432, Sequence 213840, Sequence 143835,
- 599 - 599 - 599 - 963 - 11	10-424-599-16142 10-225-066A-86 10-225-067-10 10-374-780A-2810 10-425-114-40629	14 US-10-011585A-167 0 US-09-864-761-33614 10 US-10-437-963-106810 16 US-10-437-963-169499 15 US-10-231-956A-154 16 US-10-231-956A-154	US-10-437-965-196028 US-10-029-386-33522 US-10-029-386-32407 US-10-424-599-226767 US-10-425-114-37363 US-10-437-963-115526 US-10-437-963-105502	-599-24094 301-1039 -003-45 -698-4702 -963-18143 -599-21384
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## ALIGNMENTS

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RESULT.

US-10-281-652-7

Sequence 7, Application US/10281652

Sequence 7, Application US/10281652

Sequence 7, Application No. US200300916681

SETTING NO. US200300916681

SETTING NO. US200300916681

SAPLICANT: STANYON, G. John

APPLICANT: BOLDOGH, Istvan

TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

FILE REFERENCE: 265.0022010

CURRENT APPLICATION NUMBER: US/09/641,803

PRIOR APPLICATION NUMBER: US/09/641,803

PRIOR PILLING DATE: 2000-08-17

PRIOR FILING DATE: 1999-08-17

SEQ ID NOS: 34

SOFTWARE: PRT

ORGANISM: Artificial Sequence

SEQ ID NOS: 34

COTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: peptide

US-10-281-652-7

QUELY MATCh

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 VLEMKFPPPPOETVT 15

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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
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                                                                                                                                                                    Score 51; DB 15; Length 289;
Pred. No. 40;
1; Mismatches 3; Indels
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19. OTHER INFORMATION: G502 Paralogous to G519
12.0-374-780A-2014
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PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/304,455
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR PILING DATE: 2002-06-14
PRIOR PRILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR PILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2014, Application US/10374780A Publication No. US20040019927A1 GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K APPLICANT: Riechmann, Jose Luis APPLICANT: Jiang, Cai-Zhong APPLICANT: Heard, Jacqueline E
; NAME/KEY: DOMAIN
; LOCATION: (10)...(155)
; OTHER INFORMATION: Conserved domain
US-10-225-068-104
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Dubell III, Arnold
Pineda, Omaira
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Ratcliffe, Oliver
Adam, Luc J
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Keddie, James
Broun, Pierre E
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                 1 VLEMKFPPPPQET 13
                                                                                                                                                                                           Query Match 63.0
Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-374-780A-2014
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                                                                                           Sequence 7, Application US/10691330
| Sequence 7, Application US/10691330
| Publication No. US20050042300A1
| GENERAL INFORMATION:
| APPLICANT: Boldogh, Istvan
| APPLICANT: Boldogh, Istvan
| APPLICANT: Hughes, Thomas K., Jr.
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF TOWERT PEPTION USE OF TO
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Pred. No. 0.00023;
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APPLICANT: JULG J.
APPLICANT: ALCAIN, JULG J.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pu, Guo-Liang
APPLICANT: Pu, Guo-Liang
APPLICANT: Pinceda, Omaira
APPLICANT: Broun, Pierre ELATED POLYNUCLEOTIDES AND
TITLE OF INVENTION: STERSS-RELATED POLYNUCLEOTIDES AND
TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
TITLE OF INVENTION WINDER: U6/10/25,068
CURRENT APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-08-09
PRIOR PELING DATE: 2001-11-19
PRIOR PELING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2002-06-14
NUMBER: FRANCE FRANCE OF WINDER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER: FRANCE PRIOR WINDER: 10/171,468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Peptides US-10-691-330-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mendel Biotechnology, Inc. APPLICANT: Reuber, T. Lynne APPLICANT: Riechmann, Jose Luis APPLICANT: Heard, Jacqueline E. APPLICANT: diang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/10225068 Publication No. US20030217383A1 GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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LENGTH: 289
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APPLICANT: RIKEN
TITLE OF INVENTION: A STRESS-RESPONSIVE PROMOTER AND A GENE CORDING FOR A STRESS-RESF
TITLE OF INVENTION: TRANSCRIPTION FACTOR
FILE REPERENCE: RFH14-024T
CURRENT APPLICATION NUMBER: US/10/495,918
CURRENT APPLICATION NUMBER: UP 2001-353038
PRIOR PILING DATE: 2004-05-18
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 166
SOFTWARE PALENT NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 17; Length 289;
Pred. No. 40;
1; Mismatches 3; Indels
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Publication No. US20030046723A1
GENERAL INFORMATION:
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-495-918-140
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69.2%;
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69.2%;
US20050009187A1
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Best Local Similarity 69.2
Matches 9; Conservative
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US-09-533-029-38
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Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2011

SOFTWARE: Patentin version 3.2

IED ID NO 314
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APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15; Length 289;
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Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR APPLICATION NUMBER: 09/606,720
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-22
PRIOR PLILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR PILING DATE: 2000-03-22
PRIOR PRIOR PRIOR DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR PRIOR PRIOR DATE: 2000-03-22
PRIOR PRIOR DATE: 2000-11-16
                                                                                           Sequence 314, Application US/10412699B Publication No. US20040045049A1 GENERAL INFORMATION:
                                                                                                                                                                      APPLICANT: Mendel Biotechnology, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/394,519
                                                                                                                                                                                                                         Fromm, Michael E.
Heard, Jacqueline E.
Riechmann, Jose Luis
Adam, Luc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creelman, Robert A
DuBell, Arnold N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Samaha, Raymond R.
Pilgrim, Marsha L.
                                                                                                                                                                                                                                                                                                                                                             Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                           u, Guo-Liang
iang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                     Pierre E.
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Best Local Similarity 69.2
Matches 9; Conservative
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US-10-412-699B-314
                                                                                                                                                                                                         Zhang, James
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Pred. No. 45;
1; Mismatches 3; Indels
APPLICANT: Samaha, Baymond
APPLICANT: Samaha, Samaha, Samaha, James
APPLICANT: Shang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Belber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-Old
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
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Best Local Similarity 69.2
Matches, 9, Conservative
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RESULT 8

; Sequence 140, Application US/10495918

RESULT 6 US-10-495-918-140

184 VTEMVMPPPPQQT 196

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Sequence 3649, Application US/10369493
; Sequence 3649, Application US/2030333675A1
; Publication No. US20303233675A1
; GENBRAL INFORMATION:
APPLICANT: Gao, Yongwei
; APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: UNMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3649
                                                                                                                                                                                                                                                                        Sequence 56806, Application US/10767701
Sequence 56806, Application US/10767701
Sequence 56806, Application No. USZO040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 56806
LENGTH: 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.0%; Score 47; DB 16; Length 179; 100.0%; Pred. No. 87; 0; Indels tive 0; Mismatches 0; Indels
                            Score 51, DB 14; Length 319;
Pred. No. 45;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: 30949255.pep
US-10-767-701-56806
                                        63.0%;
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ORGANISM: Neurospora crassa
                                                                                                                                                                     184 VTEMVMPPPPQQT 196
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                               1 VLEMKFPPPPQET 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Sorghum bicolor
                                             Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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US-10-278-536-148
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                                                                                                                                                                                                                                                                                                          APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
APPLICANT: Samaha, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
TITLE OF INVENTION BOATE: 2002-11-01
CURRENT APPLICATION NUMBER: 60/125,814
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beard, Jacqueline
APPLICANT: Jiang, Cal-Zhong
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Rechmann, Jose-Luis
APPLICANT: Rechmann, Jose-Luis
APPLICANT: Rechmann, Jose-Luis
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Broun, Pierre
FILE REFERENCE: MBL-01
CURRENT PILING DATE: 1999-03-23
RIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 148
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10278536
5. US20030131386A1
              US-10-286-264-22; Sequence 22, Application US/10286264; Sequence 12, Application No. US20030093837Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G502
                                                                                                       APPLICANT: Reddie, James
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Ratcliffe, Oliver
APPLICANT: Chang, James
APPLICANT: Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                   Pineda, Omaira
Heard, Jacqueline
Yu, Guo-Liang
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: G502
US-10-286-264-22
                                                                                                                                                                                                                                                                                         APPLICANT: Adam, Luc
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Sequence 20767, Application US/10424599

Bublication No. US2004001072A1

GENERAL INFORMATION:

APPLICANT: Avoil of David K
APPLICANT: Eas From Thomas J
APPLICANT: Avoil of David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220767

LENGTH: 61
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
IER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =
IER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
IER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
IER INFORMATION: EXPRESSED IN HELACON, SIGNAL = 2.5
IER INFORMATION: EXPRESSED IN HALLOW, SIGNAL = 2.5
IER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
IER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
IER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
IER INFORMATION: EXPRESSED IN BTAIN, SIGNAL = 2.6
IER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 2.8
IER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 2.8
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US-10-424-599-220767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 15;
Pred. No. 77;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 9;
Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO AC010906.2
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ilarity 87.5%;
Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MOTHER INFORMATION: EOTHER INFORMATION:
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OTHER
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US-VS-804-TOL-3/LS-95, Application US/09864761

PRECENT NO. US20020048763A1

GREREAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Rarrel, David R.

APPLICANT: APPLICANT: Chen, Wendheng

ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PRILING DATE: 2000-05-26

PRIOR PRILING DATE: 2000-06-26

PRIOR PRILING DATE: 2000-09-27

PRIOR PRILING DATE: 2000-09-27

PRIOR PRILING DATE: 2001-01-04

PRIOR PRILING DATE: 2001-01-04

PRIOR PRILING DATE: 2001-01-04

PRIOR PRILING DATE: 2001-01-04

PRIOR PRILING DATE: 2001-01-03

PRIOR PRINCE DATE: 2001-01-03

PRIOR PRILING DATE: 2001-01-03

PRIOR PRINCE DATE: 2001-01-03

PRIOR PRINC
                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Evoalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 158309
LENGTH: 56
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Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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                                                                                                                                                                                                                               Sequence 158309, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.64;
                                                                 1089 LSLSPPPPPPPT 1102
             2 LEMKFPPPPQETVT 15
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Matches 7; Conservative
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16 VLKIKIPPPRK 27
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ORGANISM: Glycine max
                                                                                                                                                                                                  US-10-424-599-158309
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US-09-864-761-37299
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14 FPPPPSET 21

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US-10-437-963-127360
; Sequence 127360, Application US/10437963
; Publication No. US2004012334341
; Publication No. US2004012334341
; Rubication No. US2004012334341
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Burbaruk, Brad
; APPLICANT: Burbaruk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Rice Nucleic Acid Molecules
; TITLE OF INVENTION: Rice Nucleic Acid Molecules
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION PLANTS
; FILE REFERENCE: 38-21(5321)8
; FILE REFERENC
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, OTHER INFORMATION: Clone ID: PAT_MRT4530_2981C.1.pep

US-10-437-963-127360
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ORGANISM: Oryza sativa
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Search completed: April 12, 2005, 07:55:22 Job time : 47.5 secs

3 EMKPPPPQE 12

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0; Gaps

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

April 12, 2005, 07:49:31 ; Search time 10.7727 Seconds (without alignments) 133.973 Million cell updates/sec

81 1 VLEMKFPPPPQETVT 15 US-10-691-330-7 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ATAF1 protein - Ar	T1N6.12 protein -	hypothetical prote	hypothetical prote	hypothetical prote	œ	DNA-binding protei	DNA-binding protei	hypothetical prote	mucin JUL10 - huma	DNA helicase Q1 in	mucin JUL7 - human	hypothetical prote	abcl protein homol	transcription fact	hypothetical prote	hypothetical prote	ч	hypothetical prote		B-cell surface ant	protein F18014.33			hypothetical prote	probable ATP-depen	C29E4.9 protein -		probable C2H2-type
QI	S37101	E86148	E84768	F83542	S24375	B86410	T52092	S26650	T29602	837595	JC5505	S35047	T39990	S71110	T09941	T26874	E87607	C86328	T22884	A46436	A30558	D86328	B87635	JX0344	E72003	D71463	S44765	0	A84549
н Б	9 2		0													09 2													0
Length	229	289	180	14	27	20	528	1203	196	33	52	54	59	61	9	7	7	15	181	18	291	440	448	47	81	91	18	21	27
& Query Match	63.0		60.5	56.8	56.8	54.3		54.3	53.1	53.1			53.1		53.1	53.1		51.9		51.9	51.9	51.9	51.9	51.9		51.9	50.6		50.6
Score	51	51	49	46	46	44	44	44	43	43	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	41	41	41
Result No.	-	7	3	4	'n	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		27		53

probable Ap2 domai	hypothetical prote	probable legumain	cell division prot	hypothetical prote	protein-tyrosine k	SSD1 protein - yea	adenomatous polypo	kinase-like protei	protein-tyrosine k	calmodulin-like pr	DedA family protei	ribosomal protein	Ig heavy chain C r	transcription regu
T01919	T36921	T12044	F81725	T15521	T23832	A39578	149505	A39712	JC4593	T49012	B75253	A48103	C30554	A84095
90	4 (4	7	~	0	7	N	N	N	~	N	N	-	~	~
287	475	493	920	1041	1196	1250	2845	1051	1070	195	202	256	308	339
50.6	20.6	20.6	9.05	9.05	50.6	9.05	50.6	50.0	50.0	49.4	49.4	49.4	49.4	49.4
41	4 4	41	41	41	41	41	41	40.5	40.5	40	40	40	40	40
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

ATARI protein - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37101
R;Rueth, J.; Schweyen, R.; Hirt, H.
R;Rueth, J.; Schweyen, R.; Hirt, H.
R;Rueth, J.; Schweyen, R.; Hirt, H.
R;Reference number: S37100
A;Reference number: S37101
A;Reference size with A;Residues: 1-229 <RUE>
A;Residues: 1-229 <RUE>
A;Residues: 1-229 <RUE>
C;Genetics:
A;Genesics: A;Genesic

Gaps ö Length 229; Indels Score 51; DB 2; Pred. No. 1.6; 1; Mismatches 63.0%; 69.2%; Query Match
Best Local Similarity 69.27

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RESULT 2

TIN6.12 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86148
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.X.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-289 <STO>

A;Cross-references: UNIPROT:Q9LQ85; GB:AE005172; NID:g8671840; PIDN:AAF78403.1; GSPDB:GN

63.0%; Score 51; DB 2; Length 289; 69.2%; Pred. No. 2.1; Query Match Best Local Similarity

A; Map position: 1

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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. A; Authors: Hunter, J.L.; V.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; C.M.; Vonter, J.C.; Davis, R.W.
A; Thie: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUD:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: Q9SGN4; GB: AE005172; NID: g6560756; PIDN: AAF16756.1; GSPDB: GN
R;Altenschmidt, U.; Bokranz, M.; Fuchs, G.
Eur. J. Biochem. 207, 715-722, 1992
A;Title: Novel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the plasmid ca
                                                                                                                                                                                                              A; Cross_references: UNIPROT: Q02304; EMBL: X66604; NID: 945865; PIDN: CAA47169.1; PID: 945867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein F3M18.20 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: B86410
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A;Molecule type: mRNA
A;Residues: 1-528 <WAN>
A;Cross-references: UNIPROT:Q9ZPL6; EMBL:AF096299; PIDN:AAD16139.1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                      Length 272,
                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                             A;Reference number: S24374; MUID:92339462; PMID:1633822
A;Accession: S24375
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-272 <ALT>
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. 16;
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7
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Pred. No. 16;
3; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 46; DB 2
Pred. No. 11;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 LRRRFPPPPDDT 164
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: F3M18.20
                                                                                                                                                                                                                                                                                         A;Genome: plasmid
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Nature 406, 959-964, 2000
A.; Filler, Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho A.; Reference number: A82950; MuID:2043737; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Moses: 1-148 <STO>
A;Cross-references: UNIPROT:0915B7, GB:AE004517; GB:AE004091; NID:g9946710; PIDN:AAG0421
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                     A, Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A, Reference number: A84420; MUD:20083487; PMID:10617197
A; Accession: B84768
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-180 <STO>
A; Cross-references: UNIPROT:082297; GB:AE002093; NID:g3608145; PIDN; AAC36178.1; GSPDB:GN
A; Genetics:
                                                                                                                                                                                                                         RESULT 3

B4768

hypothetical protein At2g35430 [imported] - Arabidopsis thaliana
hypothetical protein At2g35430 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84768
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Ahaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eus, D.; Marerman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999.
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hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740
c;Species: Pseudomonas sp.
C;Decies: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: S24375
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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Pred. No. 5.7;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2; Length 180;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                      Indels
                                         3;
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                                           Mismatches
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100 ELRLPPPPPNWQETVT 116
                                              7;
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Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                         184 VTEMVMPPPPQOT 196
                                                                                             1 VLEMKFPPPPQET 13
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                                                 9; Conservative
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VVEMKFPPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PA0822
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                                                      Matches
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A,Cross-references: UNIPROT:Q14882; EMBL:X74956; NID:g407052; PIDN:CAA52911.1; PID:g4070 R; Dufosse, J.; Porchet, N.; Audie, J.P.; Guyonnet Duperat, V.; Laine, A.; van-Seuningen, Bochem. J. 293, 329-337, 1993 A; Title: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic alternati A,Reference number: S35047; MUID:93343858; PMID:7916618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JC5505
R;Seki, T.; Tada, S.; Katada, T.; Enomoto, T.
Biochem. Blophye. Res. Commun. 234, 48-53, 1997
A;Title: Cloning of a CDNA encoding a novel importin-alpha homologue, Qipl: Discriminati A;Reference number: JC5505; MUID:97312517; PMID:9168958
A;Accession: JC5505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:000629; DDBJ:AB002533; NID:g1944124; FIDN:BAA19546.1; PID:g1
C;Comment: This protein interacts with the nuclear localization signal motif of SV40 T a
C;Superfamily: pendulin
F;ll-51/Region: importin-beta binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA helicase Q1 interacting protein 1 - human N;Alternate names: nuclear localization signal receptor importin-alpha homolog C;Species: Homo sapiens (man) C;Species: O2-Sep-1997 #sequence_revision O5-Sep-1997 #sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                        A;Introns: 40/3; 66/2; 105/2; 148/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK816.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
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                                                                                                                                                                                     Length 196;
                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.1%; Score 43; DB 2; 77.8%; Pred. No. 38; iive 1; Mismatches
                                                                                                                                                                             Score 43; DB 2;
Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aubert, J.

ubmitted to the EMBL Data Library, September 1993
,Reference number: S37593
,Accession: S37595.
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                                                                                                                                                                                     53.1%;
                                                                                                                                                                             Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          : ||||| ||
19 QFKFPPPTQE 28
                                                                                                                                                                                                                                                                                                                                          3 EMKFPPPPQE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: S37595; S35048
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <AUB>
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-330 <DUF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                A;Gene: CESP:ZK816.4
A;Introns: 40/3; 66/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Medecule type: mRNA
A; Residues: 1-1203 cMxT>
A; Cross-references: BNBL:X63071
A; Cross-references: CNBL:X63071
A; Cross-references: CNBL:X63071
A; Cross-references: CNBL:X63071
Mol. Biol. (Mosk.) 22, 794-801, 1988
A; Title: Determination of the nucleotide sequence of the human genome son3 fragment: ide
A; Reference number: RN0099; MUID:89039788; PMID:3054499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 'K',574-699,'PH',702-1055 <BER>
A; Experimental source: embryo
A; Note: this paper is in Russian, with an English abstract
B; Berdichevsky, F.B.; Chumakov, I.M.; Kiselev, L.L.
R; Berdichevsky, F.B.; Chumakov, I.M.; Kiselev, L.L.
A; Title: Determination of the nucleotide sequence of the son3 fragment of the human gency.
A; Reference number: 157397
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
326650
DNA-binding protein 5 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 01-Dec-2000
C;Accession: S26650; PM0099; I57397
R;Mattioni, T; Hume, C.R.; Konigorski, S.; Hayes, P.; Osterweil, Z.; Lee, J.S.
Chromosoma 101, 618-624, 1992
A;Title: A cDNA clone for a novel nuclear protein with DNA binding activity.
A;Reference number: S26650; MUID:93048367; PMID:1424986
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29602
R;Nhan, M: 16, T.
Submitted to the EMBL Data Library, November 1995
S;Nhan, M: 16, T.
Submitted to the EMBL Data Library, November 1995
A;Pescription: T79602
A;Pecsesion: T29602
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-196 <NHA>.
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A;Residues: 'R',574-699,'PH',702-1055 <RES>
A;Cross-references: GB:M36428; NID:g338289; PIDN:AAA36624.1; PID:g338290
C;Genetics:
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                                                                    54.3%; Score 44; DB 2; Length 528; 70.0%; Pred. No. 46; ive 2; Mismatches 1; Indels
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C;Keywords: DNA binding
F;741-928/Region: arginine/serine-rich repeats
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585 EKEVPPPKETL 596
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                                                                                                                                                                                                                             6 FPPPPQETVT 15
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79 FPPPEMTVS 88
                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
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A; Gene: WRKY2
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Length 610; 2; Indels

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Nighternate names: Vpl homolog
Cispecies: Craterostigma plantagineum
Cispecies: Craterostigma plantagineum
Cipacession: T09941
Cipacession: T09941
Cipacession: T09941
Mol. Genet. J.W.; Bartels, D.
Mol. Genet. 256, 539-546, 1997
A; Pitle: Structure and function of the Vpl gene homologue from the resurrection plant Crain Manages. 216899; MUID:98075359; PMID:9413438
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A;Cross-references: UNIPROT:023774; EMBL:AJ000552; NID:g2288898; PIDN:CAA04184.1; PID:g2
A;Experimental source: seed
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D. submitted to the EMBL Data Library, September 1998
A; Reference number: Z21906
A; Accession: T40121
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-610 <WOO>
A; Cross-references: EMBL; AL031788; PIDN: CAA21176.1; GSPDB: GN00067; SPDB: SPBC2D10.18
A; Experimental source: strain 972h-; cosmid c2D10
C; Genetics:
A; Gene: abc1; SPBC2D10.18
A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 2,
Pred. No. 75;
5; Mismatches:
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ne : 11.7727 secs
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562 MLDLRLQPPEET 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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C, Function:
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C, Species: Schizosaccharomyces pombe
C, Species: Schizosaccharomyces pombe
C, Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C; Accession: S71111, 740121, S71110
R; Bonnefoy, N.; Kermorgant, M.; Brivet-Chevillotte, P.; Dujardin, G.
R, Fulle: Cloning by functional complementation, and inactivation, of the Schizosaccharom A; Reference number: S71111; MUID:96242153; PMID:8668131
A; Reference number: S71111; MUID:96242153; PMID:8668131
A; Residues: nucleic acid sequence not shown
A; Rolecule type: mRNA
A; Residues: 177-610 < ROW>
A; Residues: 177-610 < ROW>
A; Rolecule type: mRNA
A; 
                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R;Date: 10-Bec-1993 #sequence_revision 10-Nov-1995 #text_change N.; Van-Seuningen,
R;Date: 10-Special S35047
A;Title: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic alternation, R;Reference number: S35047; MUID: 93343858; PMID: 7916618
A;Accession: S35047
A;Wolecule type: mRNA
A;Residues: 1-543 < DUFA
A;Residues: 1-543 < DUFA
A;Rosidues: 1-543 < DUFA
A;Rosidues: 1-543 < DUFA
A;Rosidues: 1-543 < DUFA
A;Rosidues: 1-543 < DUFA
A;Rote: the authors translated the codon AAA for residue 63 as Gln and CGG for residue 3
A;Note: the authors translated the codon AAA for residue 63 as Gln and CGG for residue 3
A;Note: the authors translated the rodon AAA for residue 63 as Gln and CGG for residue 3
A;Note: the amino acid sequence from Fig. 2 is inconsistent with the nucleotide sequence
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A;Nolecule type: DNA
A;Nolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: UNIPROT:O74354; EMBL:AL031158; PIDN:CAA20098.1; GSPDB:GN00067; SPDB:A;Experimental source: strain 972h-; cosmid c25D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPBC25D12.02c - fission yeast (Schizosaccharomyces pombe)

(Species: Schizosaccharomyces pombe
(Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
(Spacession: T3990
(Spacession: T3990)
(Species T3000)
(Species T300
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Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels
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0; Mismatches
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A,Map position: 2
A,Introns: 48/2
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SEQUENCE 1464 AA;
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=5141;
                                                                                                                                                                                                                                                        Name=NCU02524.1
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Query Match
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                                                           April 12, 2005, 07:49:31 ; Search time 71.1818 Seconds (without alignments) 107.909 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                 Description
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Q99j35
Q92k87
Q915b7
Q02304
Q78266
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09f183
014155
09c5i3
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0000505
035344
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P87502
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Q9gk20
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                    1612378 seqs, 512079187 residues
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Q9W0Z6
Q9F183
ARH7 HUMAN
Q9C5I3
Q8IYL7
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Q8IYQ9
Q6IRB7
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Maximum Match 100%
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092KS7
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Match Length DB
                                                                                                   US-10-691-330-7
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Calagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bitis T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Oui D., Ianakiev P., Redersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kohe G.O., Jedd G., Newses W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Bartett R., Gnerre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krytofova S., Rasmussen C., Merzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Merzenberg R.L., Perkins D.D., Kroken S., Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Varden O., Plamann M., Seller S., Dunlay J., Radicord A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Nature O.10-0(2003).

Nature O.10-0(2003).

ENBL/Genbank/DbbJ whole genome shotgun (WGS) entry which is ENBL/Genbank/DbbJ whole genome shotgun (WGS) entry which is
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felis silve
felis silve
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caenorhabdi
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
Q81ws8
Q81zz7
Q7z5r6
Q7z5r6
Q61z12
Q66pke
Q91fx0
Q6qzq3
Q94zq3
Q93f20
Q93f10
Q23f10
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Last sequence update)
Last annotation update)
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SON HUMAN
Q91FX0
Q6QZQ3
Q6QZQ2
Q6QZQ2
Q9GKZ2
Q63401
Q23610
Q14882
                         081227
0725R6
08T2L2
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EMBL; AABX01000002; EAA36419.1; -.
HSSP; Q07966; 1AM4.
InterPro; IPR001849; PH.
InterPro; IPR001036; PH related.
InterPro; IPR000198; RhoGAP.
InterPro; IPR008936; Rho_GAP.
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Pfam; PF00620; RhoGAP; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS50238; RHOGAP; 1.
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666
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1365
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dimerization domain.

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EQUINCE FROM N.A.

REGULARIES COlumbia;

X. MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;

X. Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Gunk C.M.,

M. White O., Aloneo J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A. Minte O., Aloneo J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A. Chung M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,

A. Chung M.K., Conn L., Chao G., Chen H., Chao B., Huizar L.,

A. Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A. Hunter J.L., Jonkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A. Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A. Langin-Hooper S., Liu Z.A., Luros G.S., Malti R., Marziali A.,

A. Lin X., Liu S.X., Liu Z.A., Luros G.S., Malti R., Marziali A.,

A. Lin S. Liu S.X., Liu Z.A., Luros G.S., Malti R., Souhey D.,

A. Sakano H., Salzberg S.L., Schwartz J.R., Sohin P., Southwick A.M.,

A. Suh H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

A. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

T. "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

C STRAINE-C. Collumbia;

X MEDLINE-22954850; Pubmed=14593172; DOI=10.1126/science.1088305;

X FRAINE-C. Collumbia;

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Rarlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

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A Miranda M., Tange C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari X.,

A Chan M.M., Tange C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari X.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

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A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Sekim., Sakurai T.,

Kamiya A., Tanse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                            039013; 09L085;
035-077-2004 (Rel. 45, Created)
25-077-2004 (Rel. 45, Last aguence update)
25-077-2004 (Rel. 45, Last annotation update)
NAC-domain containing protein 2 (ANACOO2)
NAC-domain containing protein 2 (ANACOO2)
Arabidopsis thaliana (Mouse-ear cress)
25-077-2004 (Rel. 45, Last annotation update)
25-077-2004 (Rel. 45, Last annotation update)
25-077-2004 (Rel. 45, Last annotation update)
NAC-domain containing protein 2 (ANACOO2)
25-077-2004 (Rel. 45, Last annotation update)
25-077-2004 (Rel. 45, Last annotation upda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ooka H., Satoh K., Doi K., Nagata T., Otomo Y., Murakami K., Matsubara. K., Osato N., Kawai J., Carninci P., Hayashizaki Y., Suzuki K., Kojima K., Takahara Y., Yamamoto K., Kikuchi S., "Comprehensive analysis of NAC family genes in Oryza sativa and Arabidopsis thaliam "; DNA Res. 10:239-247(2003).

--- DOMAIN: The NAC domain includes a DNA binding domain and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEGUENCE FROM N.A.
Ruch J., Schweyen R., Hirt H.;
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      289 AA.
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 302:842-846(2003)
                            546 LEVKMSPPPQETVS 559
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                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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                 this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,

Rounsley S.D., Lin X., Faser C.M., Somerville C.R., Venter J.C.;

Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1; Length 289;
Pred. No. 20;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                      InterPro; LEANNIN, 1.
Prom; Pro2365; NAC; 1.
PROSITE; PS51005; NAC; 1.
DNA-binding; Nuclear protein; Transcription regulation.
DNA-binding; 7
158
NAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein At2g35430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 2;
Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 AA.
-1- SIMILARITY: Contains 1 NAC domain.
                                                                                                                                                 EMBL; X74755; CAA52771.1; ALT_INIT.
EMBL; AC009273; AAF78403.1; --
EMBL; AF370617; AA843936.1; --
PIR; E86148; E86148.
PIR; S37101; S37101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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58.8%;
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Local Similarity 69.2%;
nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 VLEMKFPPPPQET 13
                                                                                                                                                                                                                                   GeneFarm; 4060; -.
InterPro; IPR003441; NAM.
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Matches
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Matches
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Rhizobium meliloti (Sinorhizobium meliloti).
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2; Mismatches
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                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Mammary tumor;
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Best Local Similarity 75.0%;
Matches 9; Conservative 1
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162 EEELPPPEEPVT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EMKFPPPPQETVT 15
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nes 8; Conservative
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                                                                                                                                                                                                                                             Strausberg R.;
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8
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                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
PubMed=14757752; DOI=10.1083/jcb.200309159;
Akazawa H., Kudoh S., Mochizuki N., Takekoshi N., Takano H., Nagai
Komuro I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                "A novel LIM protein Cal promotes cardiac differentiation by association with CSX/NKX2-5";
J. Call 1. 164:35-405 (2004).
- SIMILARITY: Contains 3 LIM zinc-binding domains.
EMBL; AF513159; AAQ08090.1; -.
HSSP; P32965; 1B8T.
InterPro; PRR001781; LIM.
Ffam; PF00412; LIM.
Probom; PD000094; LIM; 3.
SWART; SM00132; LIM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.0%; Score 47; DB 2; Length 375; 61.5%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00478; LIM DOWAIN 1; 3.
PROSITE; PS00423; LIM-DOMAIN 2; 1.
LIM domain; Metal-binding; Zinc.
SEQUENCE 375 AA; 41069 MW; 9BF3EDD16F0FA061 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                     Last sequence update)
Last annotation update)
                                                           375 AA
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                                                                                                  Created)
                                                           PRT;
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                                                     Q71FD7 PRELIMINARY;
Q71FD7;
05-JUL-2004 (TEMBLEEL: 27,
05-JUL-2004 (TEMBLEEL: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
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162 ERELPPPEEPVT 174
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                                                                                                                                                                                                Mus musculus (Mouse)
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Name=2410043F08Rik;
                                                                                                                                                            CSX-associated LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Query Match

RESULT 4

10 20.1 FP

AC 07.1 FF

DT 05-J

DT 05

Matches

ò 셤 099335

RESULT 5
099J35
10 099J35
10 01-J1
DT 01-J1
DT 01-M
DT

ö ö Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kraywinski W.I., Skalska U., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Gaps Gaps ö ö Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Contains 3 LIM zinc-binding domains.

REMBL, BCOG4777; AAH04777.1; -.

RESP, P32965; 1BR.

RIGHEPPO; 1PR001345; CytC_heme_BS.

RIGHEPPO; 1PR001345; CytC_heme_BS.

RIGHEPPO; 1PR001341; LIM.

R Pfam, PF00412; LIM; 3.

R PROSITE; PS00193; LIM; 3.

R PROSITE; PS00193; LIM; 3.

R PROSITE; PS0193; LIM DOMAIN 1; 3.

R PROSITE; PS0193; LIM DOMAIN 1; 3.

R PROSITE; PS0193; LIM DOMAIN 2; 1.

R PLIM domain; Metal-binding; Zinc.

SEQUENCE 375 AA; 41026 MW; 601DF99A8EBIBB80 CRC64; Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium. Score 47; DB 2; Length 526; Pred. No. 1.4e+02; 1; Mismatches 2; Indels 58.0%; Score 47; DB 2; Length 375; 61.5%; Pred. No. 99; Indels 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypotheital protein SMC00336.

Gaps

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Adjagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., and adjagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Rehman B., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Rothe G.O., Jedd G., Mewses W., Staben C., Marcotte E., Greenberg D., Kothe G.O., Jedd G., Mewses W., Staben C., Marcotte E., Greenberg D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Narden O., Plamann M., Seiler S., Dunlap J., Voelker R., Aramayo R., Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., The Genome Sequence of the Filamentous Fungus Neurospora crassa.;

I. Nature O.O-O(2003).

C. -- CAUION: The sequence shown here is derived from an Embly Genbank (DDBJ whole genome shotqun (WGS) entry which is Embly Genbank (DDBJ whole genome shotqun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%; Score 46; DB 2; Length 1477, on n%; Pred. No. 6.18+02; Indels
                                                                              56.8%; Score 46; DB 2; Length 272; 58.3%; Pred. No. 98;
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                                                                                                                          3; Indels
                         Ligase; Monooxygenase.
SEQUENCE 272 AA; 30631 MW; 1776F7C19A429050 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  PRT; 4587 AA.
                                                                                                                                                                                                                                                                                                                           PRT; 1499 AA.
PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
EMBL; AABX01000430; EAA29487.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
Fat 1 cadherin (Fragment).
Name-Path; Synonyms-mfatl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02213; GYF; 1.
PROSITE; PS50829; GYF; 1.
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                                                                                                                                                                                                                      153 LRRRFPPPPDDT 164
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                                                                                                                                   Conservative
                                                                                                                                                                            2 LEMKFPPPPQET 13
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SEQUENCE 1499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5141;
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Q9QXA3;
                                                                                                                                                                                                                                                                                                                                     978266
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Q9QXA3
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Q7S266
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Altenschmidt U., Bokranz M., Fuchs G.;
Altenschmidt U., Bokranz M., Fuchs G.;
Invovel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the plasmid aerobic 2-aminobenzoate for the flavoprotein 2-aminobenzoyl-CoA monooxygenase/reductase in a denitrifying Pseudomonas sp.";
Eur. J. Biochem. 207:715-722(1992).
EMBL; X66604; CA475.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
InterPro; IPR001209; Ribosomal_S14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STOWER C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Brody L.L., Goller S.N., Polger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAF-2004 (TrEMBLrel. 26, Last annotation update)
Plasmid DNA for 2-aminobenzoate-CoA ligase, 2-aminobenzoyl-CoA
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hypothetical protein.
SEQUENCE 148 AA; 16617 MW; EB8056036D1CBA4F CRC64;
                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                             148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                             PRT;
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Bacteria; Proteobacteria.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                       Hypothetical protein.
OrderedLocusNames=PA0822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.0
Matches 8, Conservative
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68 LILKFPPLPQET 79
                                         2 LEMKFPPPPQET 13
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                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
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Pfam; PF05707; Zot; 1.
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RESULT 8

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RESULT 7 09155 001515 001515 001515 001515 001515 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 00151 0015

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Gaps

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Length 1499;

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WEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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MEDLINE=22426070; Pubmed=12537573;
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   M MSSP; POS/091 16F9;

R GO; GO:0030054; C:cell junction; IDA.

R GO; GO:0030054; C:cell junction; IDA.

R GO; GO:0030027; C:lamellipodium; IDA.

R GO; GO:0030027; C:lamellipodium; IDA.

R GO; GO:0005115; F:protein binding; IPI.

R GO; GO:0007163; P:establishment organization; IMP.

R GO; GO:0016337; P:cell-cell adhesion; IMP.

R GO; GO:0016337; P:establishment and/or maintenance of cell po. ..; IMP.

R InterPro; IPR009942; GCDA_like_lec_gl.

R InterPro; IPR009424; EGF_Z.

R InterPro; IPR009129; EGF_Z.

R InterPro; IPR009129; GFOW_fac_recept.

R InterPro; IPR009129; TSP_N.

R InterPro; IPR0013129; TSP_N.

R InterPro; IPR0013129; TSP_N.

R Ffam; PF00210; Laminin_G.

R Pfam; PF00210; Laminin_G.
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                                                                                                    TISSUE=Whole embryo;
MEDLINE=20303461; PubMed=10741417;
MEDLINE=20303461; PubMed=10741417;
DDI=10.1002/(SICI)1097-0177(200003)217:3<233::AID-DVDXI>3.0.CO;2-O;
COX B.T.M., Hadjantonakis A.K., Collins J., Magee A.I.;
"Cloning and expression throughout mouse development of mfatl a homologue of the Drosophia tumour suppressor gene fat.";
Dev. Dyn. 217:233-240(2000).
-!- SIMILARITY: Contains 33 cadherin domains.
EMBL; AJSO768; CAB65271.1; --
HSSP; P08709; 18F9.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.8%; Score 46; DB 2; Length 4587; 63.6%; Pred. No. 2e+03; ive 2; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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PROSITE; PS00263; CADHERIN 2; 33.
PROSITE; PS00022; EGF 1; UNKNOWN 2.
PROSITE; PS50025; EGF 3; 4.
PROSITE; PS50025; LAM G DOMAIN; 1.
Calcium: Calcium-binding.
NOW TER
SEQÜENCE 4587 AA; 506042 MW; 4D3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00112; CA; 33.
SMART; SM00179; BGF CA; 1.
SMART; SM00282; LamG; 1.
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Best Local Similarity 63.0
Best Local 7; Conservative
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                                                    NCBI_TaxID=10090;
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Q9W0Z6,

OSCORE ELECTRONS OSCORE OSCORE

RESULT 11 ·

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.H., Blazel's K.G., Change M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C. Baxter E.G., Helt G., Nalson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Baul A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Bence P.V., Barnan B.P., Bhandari D., Bolshakov S.,
Rokova D., Botchan M.R., Boutler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., balke C., Davenport L.B., Davies P., Man
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Chorbin K.J. Evangeliste C.C., Ferraz C., Ferriac S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L.
RA Hostin D., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Harvey D., Hehman T.J., Weil M.H., Ibegwam C.,
AJalli M., Kalush F., Karpen G.H., Ke Z., Kennigon J.A., Ketchum K.A.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
ALIARO P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alasko P., Lei Y., Morinceh T.C., Mcracod M.P., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Marsiy D.M., Nelson D.L.,
Ra Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Regele M.G.,
Reinert K., Reinington K., Saunders R., Vencre E., Wassaman D.A., Weinsenbach J.,
Milliams S.M., Woodager, Worley K.C., Wall W., Yang S., Yao Q.A., Ye J.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sahe H.,
Stiener E., Spradling A.C., Sianger B., Shue B.C., Siden-Kamos I. Simpson M., Shu Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., Venter C., MEDLINE=2446065; PubMed=12537568;
MEDLINE=2446065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Batel S., Adams M., Change M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Murny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfelifer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.
Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.,
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002). MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., "Annotation of the Drosophila melanogaster euchromatic genome: a genomics perspective."; Genome Biol. 3:RESBARCH0084-RESBARCH0084(2002).

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SSUE=Amygdala;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protain (Fragment)
Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Wautersia.
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Homo sapiens (Human).
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                                                                                                                                                               Ouery Match 55.6%; Score 45; DB 2; Length 114; Best Local Similarity 77.8%; Pred. No. 54; Msmatches 0; Indels Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinner I.-S., Buerger S., Schloemann M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF042280; AAG42031.1; -.
InterPro; IPR001466; Beta lactamase.
Pfan; PF00144; Beta-lactamase;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NÔN TER 389 389
SEQÜENCE 389 AA, 42244 MW; 600D57AE93338113 CRC64;
                                                                                         Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                     FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                           C9481842A9EDE0BB CRC64;
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MEDLINE=96127530; PubMed=8590280;
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                                                                                                                                  FlyBase, FBgn0035071; CG15859.
SEQUENCE 114 AA; 11621 MW;
                                                                                                       EMBL; AE003465; AAF47282.1;
Intact; Q9W0Z6; -
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24 LDAGFPPPPDKLIT 37
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                         7 PPPPQETVT 15
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           [5]
SEQUENCE FROM N.A.
                                                                       SEQUENCE FROM N.A.
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Q9F183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REQUENCE FROM N.A. (ISOFORMS 1; 2 AND 4).

RESQUENCE FROM N.A. (ISOFORMS 1; 2 AND 4).

RESQUENCE FROM N.A. (ISOFORMS 1; 2 AND 4).

REPLINE=2238825; PubMed=12477932; DOI=10.10/3/pnas.242603899;

RA Strausberg R.L., Felngold B.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Felngold B.A., Grouse L.H., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Haieh P.N.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleron M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hidting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Repervation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse CDNA sequences.";
and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Acts as a RACI guanine nucleotide exchange factor (GEF)
and can induce membrane ruffling (By similarity).
-!- SUBUNIT: Interacts with PAK kinases through the SH3 domain.
Interacts with GIII (By similarity).
-!- ALTENNATIVE PRODUCTS:
                                                                           Ω.
Q
                                                                                                                                                                                                                                                                                       [2]
MEDLINEE=98395067; PubMed=9726964; DOI=10.1074/jbc.273.37.23633;
MEDLINEE=98395067; PubMed=9726964; DOI=10.1074/jbc.273.37.23633;
MEDLINEE=98395067; PubMed=9726964; DOI=10.1074/jbc.273.377.23633;
Manovel regulator of p21-activated kinases.";
Manovel regulator of p21-activated kinases.";
J. Biol. Chem. 273:23633-23636(1998).
Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.; Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced analysis of cDNA clones from human cell line KG-1."; DNA Res. 2:167-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wambutt R., Heubner D., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoid=Q14155-1; Sequence=VSP_011032, VSP_011035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=Q14155-3; Sequence=VSP 011034;
-!- SIMILARITY: Contains 1 CH domain.
-!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q14155-2; Sequence=VSP_011033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q14155-4; Sequence=Displayed;
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EMBL; AL834228; CAD38906.1; ALT_INIT.
EMBL; BC033905; AAH33905.1; --
EMBL; BC050521; AAH50521.1; ALT_INIT.
EMBL; BC060776; AAH60776.1; --
PDB; 1BX1; NMR; A=81-289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
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Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Cheu K., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Peki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2138424; PubMed=11487705;
Ohta M., Matsui K., Hiratsu K., Shinshi H., Ohme-Takagi M.;
Napression domains of class II ERF transcriptional repressors share an essential motif for active repression.";
Plant Cell 13:1959-1968(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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transcription, DNA-dependent; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee of Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G. Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Theologis A., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
Peldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takagi M.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF360232; AAK25942.1; -.
EMBL; AB055882; BAB62911.1; -.
                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 AA; 18612 MW; A327522DB20E5984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
APBBIIP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.3%; Score 44; DB 2; I 60.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AA
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PRINTS, PR00347; ETHRSPELEMNT.
PRODOM; PD001423; TF_ERF; 1.
SMART: SM00380; AP2; 1.
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156 LDLNFPPPPE 165
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Best Local Similarity
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Name-Atig28370; Synonyms-AtERFil;
Arabidopsis thaliama (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
8thylene-responsive element binding factor, putative (ERF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PH.
Missing (in isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (In isoform 2).
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Missing (In isoform 3)
/FTId=VSP 011034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-structure; Alternative splicing;
Guanine-nucleotide releasing factor; SH3 domain.
DOMAIN 1 132 CH.
                                                                                         H-InvDB; HIX0011460; -...
MIM; 605477; -...
GO; GO:0007165; P:8ignal transduction; TAS.
InterPro; IPR001331; GDS CDC24.
InterPro; IPR001849; PH.—
InterPro; IPR010184; PH.—
InterPro; IPR010181; RhoGEF.
InterPro; IPR001219; RhoGEF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Pfam; PF00169; PH; 1. |
| Pfam; PF00169; PH; 1. |
| Pfam; PF00621; RhoGEF; 1. |
| Pfam; PF00018; SH3; 1. |
| ProDom; PD000066; SH3; 1. |
| SWART; SW0023; PH; 1. |
| SWART; SW00225; RhoGEF; 1. |
| SWART; SW00326; SH3; 1. |
| PROSITE; PS00741; DH 1; FALSE_NEG; PROSITE; PS50010; DH 2; PROSITE; PS50003; PH_DOMAN; 1. |
| PROSITE; PS50003; PH_DOMAN; 1. |
| PROSITE; PS50002; SH3; 1. |
| PROSITE; PS50002; PH_DOMAN; PH_
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TISSUE-Blood;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodesynen E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodesynen E.J., Lu X., Gibbs R.A.,

A Wilting M.M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Razywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Gones S.J., Marra M.A.,

"Mederation and initial analysis of more than 15,000 full-length human
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54.3%; Score 44; DB 2; Length 172;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg N.; Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases. Submitted (UUL-2002) to the EMBL/GenBank/DDBJ CATABASES. EMBL; BC035636; AAH35636.1; -. SEQUENCE 172 AA; 18685 WW; 21314883C4E8C7B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S
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                                                   SEQUENCE FROM N.A.
NCBI_TaxID=9606;
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Search completed: April 12, 2005, 08:05:48 Job time : 73.1818 secs

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                                                                                           April 12, 2005, 07:49:31 ; Search time 84 Seconds (without alignments) 69.064 Million cell updates/sec
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Adn40022 Cancer/an Aau31755 Novel hum Aau75109 Clathrin Ada50752 Human cla	100010	Human Human Human Human	Aao04769 Human pol Aao1266 Human pol Aau2583 Human G P Abb93955 Herbicida Abb55121 Lactococc Aao06528 Human pol Adn47517 Thermococ
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## ALIGNMENTS

The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations. Gaps ö Length 15; Indels Dermatological; oxidative stress regulator; colostrinin. Query Match 100.0%; Score 82; DB 4; I Best Local Similarity 100.0%; Pred. No. 6.2e-07; Matches 15; Conservative 0; Mismatches 0; Boldogh I; AAB72507 standard; peptide; 15 AA Claim 6; Page 25; 48pp; English. 17-AUG-2000; 2000WO-US022665 99US-0149310P (first entry) (TEXA ) UNIV TEXAS SYSTEM Stanton GJ, Hughes TK, Colostrinin peptide #8 WPI; 2001-218342/22.

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21-MAR-2001

AAB59313;

RESULT 2 AAB5931

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Ovis sp.

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Sequences AAB72246 - AAB7225 represent peptides derived from clostrinin, ab politic rich polypeptide aggregate contained in colostrum. The peptides have immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing inducing production, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders, mental disorders, dementia, neurodegenerative diseases, Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic disorders of the immune system, bacterial and viral infections and acquired immunological deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective; neural cell differentiation regulator; colostrinin;
dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.
                                                                                                                                                                                                                                                                                                                                                   Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
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ilarity 100.0%; Pred. No. 6.2
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                      W0200111937-A2
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                                                                                                                                           22-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB72539;
                                                                                                                                                                                                                                                                                                                                                                                                                        regulator.
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                                                                        Synthetic
                                                                                                                                                                                                                                                                   (REGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder;
                                                                                                                                                                                                                                                                                       Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senila dementia, Parkinson's disease, Alzhaimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colostrinin derived cytokine inducing peptide SEQ ID 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 82; DB 4; I 100.0%; Pred. No. 6.2e-07; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                             Ewe colostrinin peptide fragment A-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB72253 standard; peptide; 15 AA.
                                                                                                                                                          AABS9313 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-00012852
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                                     LKPFPKLKVEVFPFP 15
                                                       Query Match
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgiades JA;
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AAB72253;

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Boldogh I;

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The present sequence is that of a colostrinin constituent peptide that is preferred for use as an immunological regulator and as a blood cell regulator in claimed methods of the invention. Methods are claimed for: inducing a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell by contact with an immunological regulator, where the cell is mammalian, including human; modulating an corganism, and the cell is mammalian, including human; modulating an corganism, and the cell by contact with the immunological regulator under conditions effective to induce a cytokine; modulating an immunological regulator under regulator is administered topically or as part of a dietary supplement, and where the immuno esponse is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting blood cells with a blood cell regulator, where the blood cells with a blood cell regulator, where the blood cells are increased in number or differentiated, and a method for modulating blood cell proliferation in a patent. A claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulation of blood cell proliferation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or
invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in
                                                                                                                                                         5; Length 15;
                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colostrinin; colostrum; immunomodulator; cardiovascular;
blood cell regulator; cytokine inducer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "optional C-terminal amidation"
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                                                                                                                                                     Score 82; DB 5; I
Pred. No. 6.2e-07;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  AAM51043 standard; peptide; 15 AA.
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(REGE-) REGEN THERAPEUTICS PLC.
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                                                                                                                                                                                                                                                                     the method of the invention
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                                                                                                                                                                                                  Conservative
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                Sequence 15 AA;
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                                                                                                                                  Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient.
                                                                                                                                                                                                                                                                 The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neural cell differentiation; neural cell regulator; colostrinin peptide; neural cell formation; proline-rich polypeptide aggregate; colostrum; neural cell treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 82; DB 4; Length 15; 100.0%; Pred. No. 6.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neural cell regulatory colostrinin peptide 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO14584 standard; peptide; 15 AA.
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                                                                                                                                                                                                                        Claim 6; Page 21; 35pp; English.
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                                                                                            WPI; 2001-226545/23
                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition which comprises a blood cell cregulator selected from colostrinin, its constituent peptide and/or regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level corgan, or organism; or for treating oxidative damage to the skin of a corgan, or organism; or for treating oxidative damage to the skin of a parameture birth or normal birth, preventing/delaying aging in a copilation, enhancing wound healing, and the reduction of side effects of patient, enhancing wound healing, and the reduction of side effects of commetic procedures. The method changes the level of an oxidiating species or in the cell, such as decreases or prevents increase in the level of in the cell, such as decreases or prevents increase in the level of amage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stress results in combanced repair, regeneration, and replacement of cells, tissues and corgans (e.g. kidney, liver, pancreas, skin, and the other internal and organs for external organs), as well as enhanced preservation of such organs for
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                                                                                                                                                                                                                                                                                                                                                               Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; oxgan; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
 cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide. Cytokines induced by this peptide in human leucocyte cultures include interferon-gamma, tumour necrosis factor-alpha, interleukin-6 and interleukin-10
                                                                                                                             Gaps
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                                                                                                 100.0%; Score 82; DB 5; Length 15; 100.0%; Pred. No. 6.2e-07;
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                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Colostrinin constituent peptide #8.
                                                                                                                                                                                                                                                           AAE20235 standard; peptide; 15 AA
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                                                                                                                      Local Similarity 100.
nes 15; Conservative
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                                                                                Sequence 15 AA;
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Modified-site
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                                                                                                            Query Match
                                                                                                                                      Matches
                                                                                                                                                                                                                                     RESULT 7
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The present invention describes the use of a modulator selected from colostrinin, its constituent peptide, its active analogue, and a colostrinin, its constituent peptide, its active analogue, and a colostrinin of these, for modulating an intracellular signaling molecule combination of these, for modulating an intracellular signaling molecule in a cell, down regulating HWE-mediated lipid peroxidation in a cell, can deducing the toxic effect of beta-amyloid or retinoic acid on a cell. The modulator has cytostatic activity, and can be used as a 4HNE colostriniator. The modulator is useful in the manufacture of a medicament for inhibitor. The modulator is useful in the manufacture of a medicament for glutathione depletion, inhibiting 4HNE-induced activation of c-Jun NH2-terminal kinases. Colostrinin, or its constituent peptide or active analogue is useful for colostrinin, or its constituent peptide or active analogue is useful for colostrinin apoptosis in a cell, protecting against DNA damage in a cell, or reducing the toxic effect of beta-amyloid or retinoic acid on a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of colostrinin for e.g. modulating an intracellular signaling: molecule in a cell, down regulating 4HNE-mediated lipid peroxidation in a cell, inhibiting apoptosis in a cell, or protecting against DNA damage in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulator; colostrinin; intracellular signaling molecule modulator; 4HNB-mediated lipid peroxidation down regulation; apoptosis inhibition; DNA damage; beta-amyloid; retinoic acid; cytostatic; 4HNB inhibitor; 4HNB-protein adduct formation reduction; 4HNB-inhibition; dilutablione depletion inhibition; p53 inhibition;
                                                                                                                                                                                                      Gaps
transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide
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                                                                                                                                               Score 82; DB 5; Length 15;
Pred. No. 6.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constituent peptide of colostrinin SEQ ID NO:8.
                                                                                                                                      100.0%; bcc 100.0%; Pred. No. c. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c-Jun NH2-terminal kinase inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN60302 standard; peptide; 15 AA.
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GEORGIADES J A.
HUGHES T K.
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUGH/) HUGHES T
(KRUZ/) KRUZEL M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOLDOGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004037851-A2
                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boldogh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN60302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEOR/
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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ADS74389;

RESULT 9

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Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized
                                                                                                                                                                                                                                                                                                                                                                    Sheep, colostrinin, proline rich polypeptide, colostrum, immune disorder, central nervous system disorder, dietary supplement, beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 82; DB 4; Length 16; 100.0%; Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                           Swe colostrinin peptide fragment derived sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE71271 standard; protein; 436 AA.
                                                                                                                                                                                            AABS9344 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-2000; 2000WO-GB002128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99GB-00012852
                                         1 LKPFPKLKVEVFPFP 15
                                                              1 LKPFPKLKVEVFPFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; novel protein; drug
                                                                                                                                                                                                                                                                                 21-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKPFPKLKVEVFPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LKPFPKLKVEVFPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human protein #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-071058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE71271;
                                                                                                                                                                                                                                        AAB59344;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                          AAB59344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a peptide that can be recovered from ovine colostrinin using the method of the invention. The invention or provides a method for the recovery of peptides (especially colostrinin) from colostrum in substantially pure, biologically active form and in high yield. The method involves mixing the colostrum with an alcohol to form an alcohol phase containing the colostrinin and a precipitate containing higher molecular weight caselns and other proteins. Best results are obtained using methanol or ethanol of at least 80% and precipitate, and the colostrinin is separated from the precipitate, and the colostrinin is separated from the alcohol, preferably by evaporation, to form a colostrinin-rich phase, which is recovered. A precipitation agent, such as ammonium sulfate, may be added to induce precipitation of the colostrinin peptides. The method is colostrinin applies on the colostrinin rich phase to induce precipitation of the colostrinin peptides. The method is generally applicable to the separation of peptides from fluids containing applier molecular weight proteins, lipids, carbohydrates and/or nucleic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          um, by
peptides
represents a synthetic constituent peptide of in be used as a modulator in the present invention.
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recovering peptides such as colostrinin from mammalian colostrum, mixing colostrum with alcohol to form alcohol phase containing per and precipitate, separating alcohol phase from precipitate, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colostrum; colostrinin; sheep; peptide purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kruzel ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 8; 1
100.0%; Pred. No. 6.2e-07;
ive 0; Mismatches 0;
                                                                                                                            Score 82; DB 8; I
Pred. No. 6.2e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilusz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ADS74389 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2003; 2003GB-00005552.
08-MAR-2004; 2004GB-00005190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-2004; 2004WO-GB001014.
                                                                                                                                                                                                                 1 LKPFPKLKVEVFPFP 15
                                                                                                                                                                                                                                          1 LKPFPKLKVEVFPFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                       Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovine colostrinin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recovering alcohol phase
                  The present sequence recolostrinin, which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-677519/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004081038-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
                                                                                  Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgiades JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-2004
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ADSTANSS 4389

ADSTAN

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Gaps

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0; Indels

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The invention comprises the amino acid and coding sequences of novel human proteins. The DNA and protein sequences of the invention are used in drugs. The present amino acid sequence represents a novel human protein of the invention.
                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of novel human proteins. The DNA and protein sequences of the invention are used in drugs. The present amino acid sequence represents a novel human protein of the invention.
                                                                                                                                                                                                                                                                                                             57.3%; Score 47; DB 7; Length 436; 61.5%; Pred. No. 20; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A gene and a protein encoded by it, used in drugs.
                                                                                                                                                                                A gene and a protein encoded by it, used in drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 189-192; 257pp; Japanese.
                                                                                                                                                                                                         Disclosure; Page 126-128; 257pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE71288 standard; protein; 867 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAZU-) ZH KAZUSA DNA KENKYUSHO
                                                                                                                         (KAZU-) ZH KAZUSA DNA KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2002JP-00049046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2001; 2001JP-00095524
                                                                                                   29-MAR-2001; 2001JP-00095524.
                                                                            29-MAR-2001; 2002JP-00049046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; novel protein; drug
                                                                                                                                                                                                                                                                                                                                                                               358 LTPYPKLKTALFP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                 1 LKPFPKLKVEVFP 13
                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human protein #42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-460885/44.
N-PSDB; ADE71226.
                                                                                                                                                    WPI; 2003-460885/44.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                             Sequence 436 AA;
                                                                                                                                                                N-PSDB; ADE71209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2002345493-A.
                                 JP2002345493-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-2002
           Homo sapiens.
                                                        03-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE71288;
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                              $$$X8X8X8X8X8X8X8X8X8X8X8X8X8X8
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Sequence 867 AA;

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Gaps ; 0

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The invention relates to a gamma-glutamyl cysteine synthetase named CCC HpGSH2 (ADPB8214) from the mechanol-assimilating yeast Hansenula HpGSH2 (ADPB8214) from the mechanol-assimilating yeast Hansenula polymorpha (also known as Pichia angusta), nucleic acid sequences polymorpha (also known as Pichia angusta), nucleic acid sequences cincenting HpGSH2 (promoter. The encoding HsGSH2 (AppB8215), and the HpGSH2 promoter. The cincention also relates to expression vectors and host Escherichia coli cells comprising the HpGSH2 coding sequence. HpGSH2 has 53% identity and CGP similarity to the Saccharomyces cerevisiae ScGship protein, 46% identity and 63% similarity to the Saccharomyces cerevisiae CG Schizosaccharomyces pombe SpGcslp protein, and 45% identity and 63% similarity to the Numan HsGSH2, like other gamma-glutamyl cysteine synthetases, is involved in the biosynthesis of glutathione, CG systeine synthetases, is involved in the biosynthesis of glutathione, CG which plays a key role in the detoxification of substances such as heavy which HpGSH2-encoding nucleic acids may be used for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel genomic DNA comprising gamma-glutamyl cysteine synthetase gene and its promoter derived from Hansenula polymorpha, useful in mass production of glutathione.
                             ö
                                                                                                                                                                                                                                                                                                                               Gamma-glutamyl cysteine synthetase; HpGSH2; methanol-assimilating yeast; Hansenula polymorpha; glutathione biosynthesis; detoxification; heavy metal; adsorption; detection; mass production; liver function; food additive; nutritional supplement; adsorption; enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= GWRVEFRPME motif
/note= "Binds glutathjone. Corresponds to SEQ ID NO:5"
503
                               Gaps
                                                                                                                                                                                                                                                                                             Hansenula polymorpha gamma-glutamyl cysteine synthetase HpGSH2.
                                 ;
 Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG. (CELL-) INST CELL BIOLOGY. (REAL-) REAL BIOTECH CO LTD. (KORI-) KORITSU KK.
DB 7;
42;
 Score 47; DB 7
Pred. No. 42;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Binds glutathione"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251. .261
/label= MGFGMGXXCLQ_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; SEQ ID NO 3; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                              ADP88214 standard; protein; 650 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2002; 2002JP-00339824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2002; 2002JP-00339824.
     57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADP88212, ADP88215.
                                                                                               | |:|||| :||
114 LTPYPKLKTALFP 126
                                                                                                                                                                                                                                                                     09-SEP-2004 (first entry)
                                                                      1 LKPFPKLKVEVFP 13
         Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-456234/43
                                                                                                                                                                                                                                                                                                                                                                                                food additive; nutri
cell growth; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2004173503-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pichia angusta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Active-site
                                                                                                                                                                                                                                       ADP88214;
                                                                                                                                                                    RESULT 13
                                                                                                                                                                                      ADP88214
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Glutathione may be used to improve liver function, as a nutritional gupplement or food additive (e.g., in sports drinks), as a decoxifying agent, as an agent for adsorption of heavy metals, and in enzyme production. The HpGSH2-encoding nucleic acids may also be used to restore cell growth function to glutathione synthesis-defective host cells. The HpGSH2 promoter may be used in reporter constructs useful in the detection of toxic substances such as heavy metals. The present sequence represents the Hansenula polymorpha gamma-glutamyl cysteine synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a pulypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                        8; Length 650;
                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                        Score 44; DB
Pred. No. 98;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 46846; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #16478.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG16487 standard; protein; 175 AA.
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                                                                                                                                                                                                                                      53.7%;
                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-00540217
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                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                     Query Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                            1 LKPFPKLKVEVFPFP
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 repressent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this spatent did not appear in the printed specification, but was obtained in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                            52.4%; Score 43; DB 4; Length 175; 61.5%; Pred. No. 35; 1, Mismatches 4; Indels
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                                                                                                                                                                                                                                                         AAG57452 standard; protein; 240 AA.
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PR 02-MuG-1999; 99US-0146389P.
PR 03-AuG-1999; 99US-0147302P.
PR 04-AuG-1999; 99US-0147302P.
PR 05-AuG-1999; 99US-0147302P.
PR 05-AuG-1999; 99US-0147302P.
PR 10-AuG-1999; 99US-0147432P.
PR 11-AuG-1999; 99US-0147432P.
PR 11-AuG-1999; 99US-0149131P.
PR 11-AuG-1999; 99US-0149132P.
PR 12-AuG-1999; 99US-0149132P.
PR 13-AuG-1999; 99US-0149132P.
PR 20-AuG-1999; 99US-0151066P.
PR 20-AuG-1999; 90US-015106P.
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PR 20-CCT-1999; 90US-015919P.
PR 20-CC

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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-016193P.
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Query Match
Best Local Similarity 61.5%; Pred. No. 49;
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Db 203 PTPHLVVEITPFP 215

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Job time: 86 secs
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Sequence 8, Appli
Sequence 16790, A
Sequence 19503, A
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Sequence 16, Appl
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-248-796A-16790
US-09-248-796A-19503
US-09-553-110-4463
US-09-555-820A-16
US-09-555-820A-14
US-09-555-820A-14
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US-09-248-796A-16790

Sequence 16790, Application US/09248796A

Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196_132

FILE REPERIORS: 107196_132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409
                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09641803

Sequence 8, Application US/09641803

Patent No. 6500798

GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: BOLDOGH, ISTVAN
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
FILE REFERENCE: 265.00220101
CURRENT PELING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
FILE REPRING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENT IN Ver. 2.1
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
CORGANISM: Artificial Sequence
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Sequence 5301, Ap
Sequence 14738, A
Sequence 1405, A
Sequence 21294, A
Sequence 21294, A
Sequence 19007, A
Sequence 1065, A
Sequence 10, Appl
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US-09-270-767-44738
US-09-228-991A-10297
US-09-252-991A-21294
US-09-248-796A-19007
US-09-248-796A-19007
US-09-949-016-6372
US-09-949-016-6372
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US-09-940-016-6372
US-08-864-785-2
PCT-US93-0306-9078-7
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Matches 15; Conservative
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Squarce 16, Application US/0955820A
Squarce 16, Application US/0955820A
Squarce 16, Application US/0955820A
Squarce 16, Application US/0955820A
GENERAL INFORMATION:
Squarce 10, Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless TILE OF PREMION: A Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless TILE OF Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless TILE OF Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elevated Levels of Starchless Variety of Pisum Sativum Having Elev
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Patent No. 6660429

Patent No. 6660429

Patent No. 6660429

APPLICANT: Webster, David

APPLICANT: Burgess, Diane

APPLICANT: Source No. 2000-08-29

CURRENT PILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

TENGTH. 46-2
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63.6%; Pred. No. 1.2e+02;
ive 1; Mismatches 3; Indels
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
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                     7; Conservative
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US-09-555-820A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pisum sativum
US-09-555-820A-16
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Sequence 4463, Application US/09583110

Batent No. 6699703

GENERAL NO. 6699703

GENERAL INCERMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: PATHOG-07A

CURRENT APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

LENGTH: 96

LENGTH: 96
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US-09-248-796A-19503
US-09-248-796A-19503
US-09-248-796A-19503
Sequence 19503, Application US/09248796A
Fatent No. 6747137
Fatent No. 6747137
FAPELCANT: Reith Wedistock et al
APPLICANT: Reith Wedistock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
FILE REPERENCE: 107196-132
GURRENT PILING DATE: 1999-02-13
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-08-13
NUMBER: US 60/096,409
NELOR FILING DATE: 1998-08-13
NUMBER: US 60/096,409
NELOR FILING DATE: 1998-08-13
NUMBER: US 60/096,409
SEQ ID NO 19503
NUMBER: US 60/096,409
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88;
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Pred. No. 24;
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Pred. No. 88;
1; Mismatches
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Best Local Similarity 66.7%;
Matches 8; Conservative
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US-09-248-796A-19503
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                                  NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16790
LENGTH: 176
                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16790
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
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US-09-583-110-4463
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstown NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US /09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
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Patent No. 6562958
GENERAL INFORMATION:
Patent No. 6562958

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: GTC99-03PA
CURRENT APPLICATION VUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 95;
  Indels
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  3,
Mismatches
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; Sequence 16764, Application US/09248796A
; Patent No. 6747137
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-5541
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Best Local Similarity 88.9
Matches 8; Conservative
  Conservative
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                                             4 FPKLKVEVFPF 14
                                                                                    33 FPSFKVQNFPF 43
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LENGTH: 346
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Sequence 12, Application US/0955820A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Webster. David
APPLICANT: Burgess, Diane
TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of FILE REFERENCE: SVS3801P0302US
CURRENT APPLICATION NUMBER: US/09/555,820A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 6.26
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TITLE OF INVENTION: ONTENT OF PLANTS
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/214,619
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                                                                                                                                                                                                Score 40; DB 4; Length 618;
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/09214619; Patent No. 6538180; GENERAL INFORMATION:
  2000-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%;
                    NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 618
                                                                                                                                                                                              48.8%;
ilarity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 626 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                       4 FPKLKVEVFPF 14
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                                                                                                         ; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-555-820A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pieum sativum
US-09-555-820A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 PPSFKVQNFPF
                                                                                                                                                                    Query Match
Beet Local Similarity
7; Conserva
  CURRENT FILING DATE:
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Best Local Similarity
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US-09-555-820A-12
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TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 6; Conserv
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STATE: Georgia
COINTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-201-945-89
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47.6%; Score 39; DB 4; Length 642;
Best Local Similarity 46.7%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-637-759B-89

1 Gacuence 89, Application US/08637759B

1 Patent No. 2876931

1 GENERAL INFORMATION:
1 GENERAL INFORMATION:
2 APPLICANT: David #111iam Holden
2 TITLE OF INVENTON: Identification of Genes
3 TREET: 2800 One Atlantic Center
3 STREET: 1201 West Peachtree Street
3 STREET: 2800 One Atlantic Center
5 STREET: 1201 West Peachtree Street
6 COUNTRY: USA
6 COUNTRY: USA
7 CONPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
7 COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIN NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: 31,284
RECISTAATION NUMBER: 31,284
RECISTAATION NUMBER: 31,284
RESPENCE/DOCKET NUMBER: 31,284
RESPENCE/DACET NUMB
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FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5199
LENGTH: 642
                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| | :| :| |
140 LKPLSKQLIEQYPLP 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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462 PLPEVNIEVLPEP 474

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Sequence 90, Application Us/08071355A

Petent No. 6015659

Return Return L. Pabet

STREET: 2010 West Packhire Street

STREET: 1201 West Packhire

STREET: 12
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Query Match
47.6%; Score 39; DB 3; Length 759;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FLING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
NAME: Pabet, Patrea L.
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,287
FELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
TELEPHONE: CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: Ineat
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-89
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Search completed: April 12, 2005, 08:07:54 Job time : 18.5909 secs

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Gaps ö

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Sequence 201195, Sequence 194, Appl Sequence 194084, Sequence 224398, Sequence 274254, Sequence 213540, Sequence 118336, Sequence 11931, Sequence 1796, Appl Sequence 11936, Sequence 1796, Appl Sequence 119859, Sequence 13888, Sequence 138888, Sequence 13888, Sequence 138888, Sequence 176411, Sequence 176411, Sequence 176411, Sequence 176411, Sequence 176411, Sequence 176411, Sequence 176421, Sequence 176421, Appl Sequence 176421, Appl Sequence 176441, Appl Sequence 176441, Appl Sequence 176421, Appl S

Sequence 1337, Ap Sequence 40273, A

Sequence 13, Appl Sequence 187658, Sequence 280508, Sequence 121736, Sequence 12, Appl Sequence 13, Appl

Perfect score: Sequence:

on:

Searched:

Database

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genence 8, Application US/10281652

Publication No. US20030091606A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
GURERY APPLICATION NUMBER: US/10/281,652
CURRENT APPLICATION NUMBER: US/10/281,652
CURRENT FILING DATE: 2002-10-28
FRIOR APPLICATION NUMBER: US/10/41,803
FRIOR PELLING DATE: 2000-08-17
FRIOR PELLING DATE: 2000-08-17
FRIOR FILING DATE: 2000-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 82; DB 14; Length 15; 100.0%; Pred. No. 2.6e-06; Live 0; Mismatches 0; Indels
S US-10-108-260A-2682

US-10-295-027-1340

6 US-10-826-909-34

US-10-424-599-139084

US-10-424-599-274398

US-10-424-599-274254

US-09-738-626-009-0

US-09-738-626-009-0

US-10-424-599-274254

US-10-424-599-274254

US-10-424-599-274254

US-10-424-599-274254

US-10-437-963-119336

US-10-437-963-11964

US-10-437-963-11966

US-10-437-963-11966

US-10-424-599-150187

US-10-424-599-150187

US-10-424-599-176441

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US-10-424-599-176451

US-10-425-114-46153

US-10-428-114-40273
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US-10-424-599-280508
US-10-437-963-121736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 15; Conservative
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LENGTH: 15
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Sequence 13568,
Sequence 14881,
Sequence 178881,
Sequence 172791,
Sequence 13758,
Sequence 13758,
Sequence 266211,
Sequence 31588,
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Sequence 64363, A
Sequence 45491, A
                                                                                                                                             April 12, 2005, 07:49:30 ; Search time 46.5 Seconds (without alignments) 107.096 Million cell updates/sec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2_6/ptodata/1/pubpaa/VSO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/RCT_MEW_PUB.pep:*

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4: \cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/NSO7_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/NSO8_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

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16: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

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17: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

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19: \cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-691-310-8
US-10-424-599-13568
US-10-437-963-178880
US-10-437-963-178880
US-10-437-963-177191
US-10-437-963-137-88
US-10-424-599-266211
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US-10-424-599-266211
US-10-424-599-266211
US-10-424-547-963-117-88
US-10-424-547-963-117-46
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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82
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Result Š.

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RESULT 4

US-10-424-599-146821

is Gquence 146821, Application US/10424599

is Gquence 146821, Application No. US20040031072A1

is Gquence 146821, Application No. US20040031072A1

is Gquence 146821

is Gquence 146821

is APPLICANT: La Rosa Thomas J

is APPLICANT: Apolication No. USA040 Molecules and Other Molecules Associated With

it TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

is TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement

is CURRENT APPLICANTON NUMBER: US/10/424,599

is CURRENT FILING DATE: 2003-04-28

is SEQ ID NOS: 285684

is SEQ ID NO 146821

LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: En Rosa, Thomas J.
APPLICANT: Shoulic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 178880
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US-10-437-963-178880
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53.3%; Pred. No. 39;
tive 3; Mismatches 4
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Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 172791, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 178880, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.1%;
Best Local Similarity 72.7%;
Matches 8; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKPFPKLKVEVFPFP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PFPKLKVEVFP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-437-963-172791
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                                                                               ## Sequence B, Application US/10691330

| Sequence B, Application US/10691330
| Publication No. US20050042300A1
| GENERAL INFORMATION:
| APPLICANT: Boldogh, Istvan
| APPLICANT: Stanton, G. John
| APPLICANT: Stanton, G. John
| APPLICANT: Stanton, G. John
| APPLICANT: Hapkes, Thomas K., Jr.
| APPLICANT: Los of COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES
| TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES
| TITLE OF INVENTION: USE OF COLOSTRININ, OUR PETITOR UNDER OF COLOSTRININ, OUR PETITOR PETITOR UNDER OF COLOSTRININ, USE OF CONSTITUENT PETITOR UNDER OF COLOSTRININ, USE OF COLOSTRININ, USE OF US
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53.23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 235568
LENGTH: 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 82; DB 17; Length 15; Best Local Similarity 100.0%; Pred. No. 2.6e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_S4835C.1.pep
US-10-424-599-235668
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LOCATION: (1)..(309)
OTHER INFORMATION: unsure at all Xaa locations
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275 LKPFAPKIPIEVFLEAIKPTLPFP 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic Peptides.
US-10-691-330-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: artificial
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US-10-424-599-266211

Sequence 266211, Application US/10424599

Publication No. US20040031072A1

SERNERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Rovalic David K

APPLICANT: Cao Yongwei

TITE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT FILING DATE: 2003-04-28

UNMBER OF SEQ ID NOS: 285684

SEQ ID NO 266211

LENGTH: 85
                                                                                                                                  APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137588
LENGTH: 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20030236392Alel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_39057C.1.pep
US-10-437-963-137588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_8240C.1.pep
US-10-424-599-266211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.8%; Score 42.5; DB 16; Best Local Similarity 60.0%; Pred. No. 6.3e+02; Matches 9; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(1515)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                  Wu, Wei
Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||| : | |||
1374 QPFPKLVFKYFGPFP 1388
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Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                          Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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Squence 3, Application US/10771931

Publication No. US20040151737A1

GREERAL INFORMATION:

APPLICANT: COURTINGY, Harry

TITLE OF INVENTION: Streptococcal Serum Opacity Factors And Fibronectin-Binding Prote

TITLE OF INVENTION: Peptides Thereof For The Treatment And Detection of Streptococca

FILE REPERIOR: 13314-1001U

CURRENT APPLICATION NUMBER: US/10/771,931

CURRENT FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
                              TITLE OF INVENTION: Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 204966
LENDIN: 1173
TYPE: POTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70893C.1.pep
US-10-437-963-172791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.5; DB 16;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(1173)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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OTHER INFORMATION: Xaa = Any Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%;
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968 RPFPKLAFKYFGPFP 982
La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KPFPKLKVEVF-PFP 15
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Best Local Similarity 60.0°
....hes 9; Conservative
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Matches 7; Conservative
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APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Shouls, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45491
LENGTH: 443
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Sequence 2682, Application US/10108260A

School-2682, Application US/20108260A

GENERAL INFORMATION:

APPLICATION HELIX RESERCH INSTITUTE

TILLE OF INVENTION: NO. US20040005560Alel full length cDNA

FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT PILLING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458
                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                      , OTHER INFORMATION: Clone ID: LIB3689-218-D2_FLI.pep
US-10-425-114-64363
                                                                                                                                                                                                                                   Score 42; DB 15; L
Pred. No. 1.9e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%; Score 42; DB 15;
54.5%; Pred. No. 2.1e+02;
tive 3; Mismatches 2;
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: 700377865_FLI.pep
US-10-425-114-45491
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-45491
; Sequence 45491, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64363
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.2%;
                                                                                                                                                                                                                                     Query Match 51.2%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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SEQ ID NO 2682
LENGTH: 554
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159 FPSLRFEIYPF 169
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ORGANISM: Homo sapiens
US-10-108-260A-2682
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Best Local Similarity
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Best Local Similarity
                                                                                                  TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS-10-425-114-64363

Sequence 64363, Application US/10425114

Fublication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Stou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabeska, Jack E

APPLICANT: Tabeska, Jack E

APPLICANT: Tabeska, Jack E

APPLICANT: Tabeska, David K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114
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Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
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Pred. No. 1.4e+02;
3; Mismatches 2; Indels
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--hog 5; Indels
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US-10-437-963-117046
       ; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117046, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.5%;
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207 LRKFPVLPVHPWPFP 221
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Best Local Similarity 54.5
Matches 6; Conservative
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US-10-104-047-3111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-437-963-117046
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APPLICANT:
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APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginaberg, Wendy
APPLICANT: Mack. David H.
APPLICANT: Mack. David H.
APPLICANT: Mack. David H.
APPLICANT: Wateon, Suan R.
APPLICANT: Soo, Suan R.
APPLICANT: Wateon, Suan R.
APPLICAN
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3; Indels
1; Mismatches
                                                                                                                                                                                                                                                                                                          Sequence 1340, Application US/10295027 Publication No. US20030232350A1 GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 8; Conservative
8; Conservative
                                                                      1 LKPFPKLKVEVF 12
                                                                                                                                        83 LDPLPSLKVEVY 94
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; ORGANISM: Homo sapiens
US-10-295-027-1340
                                                                                                                                                                                                                                               RESULT 15
US-10-295-027-1340
   Matches
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479 LDPLPSLKVEVY 490 g

1 LKPFPKLKVEVF 12

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0; Gaps

Search completed: April 12, 2005, 07:55:22 Job time : 46.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 12, 2005, 07:49:31 ; Search time 10.7727 Seconds (without alignments) 133.973 Million cell updates/sec Run on:

US-10-691-330-8 82

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 LKPFPKLKVEVFPFP 15 Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein F19P19.17	hypothetical prote	probable receptor-		hypothetical prote	ರ	oxidoreductase ord	hypothetical prote	hypothetical prote	C02D5.3 protein -	clathrin heavy cha	probable cystathio	extracellular solu	hypothetical prote	hypothetical prote	e pro	probable metal bin	probable metal bin	probable membrane	hypothetical prote			hypothetical prote		Ω	probable 4-hydroxy			
SUMMARIES	ID	F86175	G90477	C84668	T45013	T28908	C97432	AD2650	T18974	T22933	S44745	LRRTH	T38233	A82221	S75790	C64432	D86846	T19157	T19156	S59393	T32913	C87723	E86233	AB2992	H98291	YXBYT	B75188	T33839		T51898
	DB	~	~		~		~					Н			7	~			7								•	7	7	7
	Length	127	790	1007	190	343	428	428	939	965	379	1675	398	401	496	537	736	1353	1424	1556	134	134	193	212	212	259	336	424	~	258
*	Query	52.4	52.4	N	51.2	51.2	51.2	51.2	51.2	51.2	50.6	50.6	50.0	50.0	50.0	20.0	20.0	50.0	50.0	49.4	48.8	48.8	48.8	48.8	œ.	48.8	•	•	48.8	47.6
	Score	43	43	43	42	42	42	42	42	42	41.5	41.5	41	41	41	41	41	41	41	40.5	40	40	40	40	40	40	40	40	40	39
	Result No.	1	7	m	4	S	9	7	80	đ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	. 27	28	59

thymidylate syntha	gamma-gliadin prec	hypothetical prote	hypothetical prote	probable rRNA meth	probable rRNA meth	probable nucleolar	receptor protein k	hypothetical prote	probable type III	hypothetical prote	hypothetical prote	heterocyst glycoli	hypothetical prote	hypothetical prote	hypothetical prote
YXMST	JS0402	D97042	G90274	C64945	A98947	E85795	T50006	T05758	AF0697	G71004	A82940	AH2011	T02345	AD1408	AD1784
г	N	N	~	~	~	~	~	~	7	~	~	N	~	~	7
307	327	371	385	481	481	481	509	562	681	206	782	1263	1791	270	270
47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.0	47.0
39	39	39	39	39	39	39	39	39	39	39	39	39	39	38.5	38.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C;Accession: F86175
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; i.J., J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome loftheplant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:022688; GB:AE005172; NID:92341037; PIDN:AAB70437.1; GSPDB:GN
protein F19F19.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 127;
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A;Molecule type: DNA
A;Residues: 1-127 <STO>
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A;Map position: 1
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1; Indels Score 43; DB 2; Pred. No. 4.8; 1; Mismatches 52.4%; 80.0%; 8; Conservative Query Match Best Local Similarity Matches

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Gaps

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1 LKPFPKLKVE 10 68 |||||||||| 59 LKPFPRLKSE g ઠે

hypothetical protein soxM [imported] - Sulfolobus solfataricus

Cispecies: Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
CiAccession: G30477
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chanarett, J.; Jeffriss, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Cost, J.

A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A99139

A;Cross-references: UNIPROT:Q97UNO; GB:AE006641; NID:g13816356; PIDN:AAK43078-1; GSPDB:G A;Status: preliminary A;Molecule type: DNA A;Residues: 1-790 <KUR>

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Similarity 64.3%;
9; Conservative
110 FPKLEKELFPEQFP 123
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Best Local Similarity
Local 8; Conserva
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Best Local Similarity
Matches 9; Conserv
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A,Molecule type: DNA
A,Residues: 1-428 <KUR>
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A;Map position: cir
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C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: C34668

R;Lin, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

Nature 402, 761-768, 1999

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Recence number: A84420; MUID:20083487; PMID:10617197

A;Residues: 1-1007 <STO>

A;Cross-references: UNIPROT:Q9ZVD4; GB:AE002093; NID:g3885336; PIDN:AAC77864.1; GSPDB:GN

A;Genetics:
C;Genetics:
A;Map position: 2
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               C,Genetics:
SoxM
A;Gene: soxM
C;Superfamily: cytochrome-c oxidase chain I/III; cytochrome-c oxidase chain I homology
C;Superfamily: cytochrome-c oxidase chain I/III; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated comple
C;Keywords: copper; electron transfer; heme; iron (His) faxtal ligands) #status predicted
F;237,289,290/Binding site: copper (His) #status predicted
F;239,289,243/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F;243/Binding site: oxygen (Tyr) #status predicted
F;375/Binding site: heme al iron (His) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>.</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.2%; Score 42; DB 2; Length 190; Best Local Similarity 64.3%; Pred. No. 11; Matches 9; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2; Length 790, Pred. No. 31; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2
Pred. No. 40;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.4
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 PPLKVEYFPLP 660
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4 FPKLKVEVFP--FP 15

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probable oxidoreductase ordl AGR C_1066 [imported] - Agrobacterium tumefaciens (strain Ct) Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: C97432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cjaccession: AD2650
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R; Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: Q8UHS8; GB: AE007869; PIDN: AAK86412.1; PID: 915155546; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:022807; EMBL:U41017; PIDN:AAC48211.1; GSPDB:GN00028; CESP:T24
A;Experimental source: strain Bristol N2; clone T26C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase ordi [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                 C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2; Length 343;
pred. No. 20;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                     C;Accession: T28908
R;Martin, J.
Bubmitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T26Cll.
A;Reference number: Z20542
hypothetical protein T26C11.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                    A;Accession: T28908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-343 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.2%; Score 42; DB 61.5%; Pred. No. 25; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position; X
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Map positīon: circular chromosome
Superfamily: hypothetical protein H10499
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Gaps

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2317-2323, 2001

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A, Molecule type: mRNA, Makeaidues 1-1675 eXIR. Makear Experiences: UNIPROT: P11442; GB: J03583; NID: 9203301; PIDN: AAA40874.1; PID: 9203302 C; Comment: Clathrin, the major protein component of coated pits and vesicles, is a three C; Comment: The amino end of the mature protein is blocked. C; Comment: The amino end of the mature protein is blocked. C; Superfamily: clathrin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kirchhausen, T.; Harrison, S.C.; Ping Chow, E.; Mattallano, R.J.; Ramachandran, K.L.; Proc. Natl. Acad. Sci. U.S.A. 84, 8805-8809, 1987
A;Title: Clathrin heavy chain: molecular cloning and complete primary structure.
A;Reference number: A39941; MUID:88097376; PMID:3480512
                                                                                                                                                                                                                                                                                                          CO2D5.3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S44745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A39941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: P34277; EMBL: L16622; NID: 9289603; PID: 9289606
     Length 965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid C02DS.
A;Reference number: 844613
A;Accession: 844745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 1.2e+02;
2; Mismatches 2;
  DB 2;
57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.6%; Score 41.5; I
66.7%; Pred. No. 26;
tive 1; Mismatches
                                                          2; Mismatches
  Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 15/1; 90/1; 174/2; 196/1; 272/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;480-523/Region: link
F;524-634/Domain: distal <DIS>
F;635-638/Region: joint #status predicted
F;639-1675/Domain: proximal <PRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: coated pits
:1-479/Domain: amino-terminal <TER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 IKDFP-LKVESFPGP 333
.51.2%;
llarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKPFPKLKVEVFPFP 15
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241 QPFPKKAVDVF-FP 253
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188 LKSLPCIKLEVFP 200
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Best Local Similarity 64...
Best Local 9; Conservative
                                                                                                              1 LKPFPKLKVEVFP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clathrin heavy chain - rat
                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-379 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: DNA
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     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
T38233
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Date.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22933
R;Smye, R.
A;Reference number: 219639
A;Reference number: 219639
A;Reference number: 219639
A;Reference number: 219639
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-965 <WIL>
A;Residues: 1-965 <WIL>
A;Cross-references: UNIPROT:O62275; EMBL:Z81556; PIDN:CAB04524.1; GSPDB:GN00020; CESP:FS
A;Experimental source: clone F58G1
C;Genetics:
                                                                                                                                                                                            A;Residues: 1-428 «KUR»
A;Cross-references: UNIPROT:Q8UHS8; GB:AE008688; PIDN:AAL41618.1; PID:g17738956; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
  A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                              A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Atele: The Canome of the Natural Genetic Engineer Agrocesion: AD2650 A;Accession: AD2650 A;Accession: AD2650 A;Accession: Ap261 A;Accession: Ap261 A;Accession: Agriculary A;Molecule type: DNA
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A;Introns: 52/3; 116/2; 172/3; 308/1; 550/2; 609/1; 665/2; 723/3; 805/3; 927/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2
A;Introns: 52/3; 116/2; 146/3; 282/1; 524/2; 583/1; 639/2; 697/3; 779/3; 901/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reaidues: 1-939 <WIL>
A;Cross-references: EMBL:Z49886; PIDN:CAA90054.1; GSPDB:GN00020; CESP:C06Al.4
A;Experimental source: clone C06Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C06Al.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18974
R;McMurray, A.
submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 55;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   core 42; DB 2; Length 428; red. No. 25; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T18974
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                    A;Map position: circular chromosome
C;Superfamily: hypothetical protein H10499
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                                                                                                                                                                                                                                                                                                                                                                                                                      51.2%;
ilarity 61.5%;
Conservative
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393 LAPFARLKVPAFP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKPFPKLKVEVFP 13
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hes 8; Conservi
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Best Local Similarity
Matches 8; Conserv
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A;Gene: CESP:C06A1.4
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A;Residues: 1-537 <BUL>
A;Cross-references: UNIPROT:Q58460; GB:U67549; GB:L77117; NID:g2826363; PIDN:AAB99072.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: C64432
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-537 <BUL>
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Pred. No. 46;
0; Mismatches
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A,Map position: FOR1000459-1002072
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tes 9; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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hypothetical protein s110827 - Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A62035; MUD:20406833; PMID:10952301
A;Accession: A62221
A;Accession: A62231
A;Accession: A62221
A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extracellular solute-binding protein, family 7 VC1273 [imported] - Vibrio cholerae (stra
C,Species: Vibrio cholerae
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: EMBL:AL021813; PIDN:CAA16988.1; GSPDB:GN00066; SPDB:SPAC23A1.14c
A.Experimental source: strain 972h-; cosmid c23A1
probable cystathionine gamma-synthase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
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                                                                                C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                     R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: Z21780
A;Accession: T38333
A;Accession: T38333
A;Status: pre-liminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 < MUR>
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A;Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 34;
2; Mismatches 3; Indels
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FPDVKVKTFPAP 347
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Best Local Similarity 58.3
Matches 7; Conservative
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A,Gene: SPDB:SPAC23A1.14c
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A,Gene: VC1273
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3; Indels

DB 2; Length 537; 46;

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A;Molecule type: DNA
A;Residues: 1-496 «KAN>
A;Cross-references: UNIPROT:Q55425; EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA1052:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein sl10827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cjacession: C64432
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.J.; White, O.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Atuthors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUID:96337999; PMID:8688087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein MJ1060 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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Pred. No. 42;
1; Mismatches 3; Indels
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SEQUENCE FROM N.A.
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D.,
                                                                                                                                                                                                                                                            Fragaria ananassa (Strawberry). Bukaryophyta, Tracheophyta, Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Rosales, Rosaceae, Rosoideae, Fragaria.
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Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUB-Receptacle;
Balogh A., Koncz T., Kiss E., Heszky L.E.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX642689; AAT66507.1; -
NON_TER 1
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SEQUENCE 70 AA, 8298 MW; DB707AS86C9EE4B9 CRC64;
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70 AA; 8298 MW; DB707AS86C9EE4B9 CRC64;
                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable mitochondrial carrier protein (Fragment).
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Last sequence update)
Last annotation update)
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Pred. No. 3.2;
1; Mismatches
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Q8NAJ2
Q992W1
Q7CF58
Q22807
Q6Z5N7
Q8UHS8
Q7MWE7
          092VD4
074ZT5
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IKLSPKLKLRIFPWP 31
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NCBI_TaxID=3747;
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                          1612378 seqs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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09VVQ7
09VVQ7
065YG6
062PH3
0948H7
0948M3
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0948L9
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0948L9
0948L9
0948L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q948L5
Q9XIV7
Q6XM21
Q6VCW5
                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                           1 LKPFPKLKVEVFPFP 15
                                                                                                                                                                                                                                                                                          1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                               seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                        US-10-691-330-8
                                                                                                                                                                                                                                                                                 UniProt 03:*
                    Copyright
                                                                                                                                              BLOSUM62
                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                              Minimum DB E
Maximum DB E
                                                OM protein
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                                                                   Run on:
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Gaps

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435 AA

Length 70; 3; Indels (MAR-2004) to the EMBL/GenBank/DDBJ databases

Submitted

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew M., Basendale J., Bayraktarogul L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Braddari D., Bolbhakov S., Brkw., Bouck J., Brokstein P., Brottier P., Borchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P., Dodgon K., Doup L.E., Downes M., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferras S., Pleishmann W., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Plankov B.C., Dunk D. B., Boolp L.E., Downes M., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Plankov B.C., Dunk D. B., Harris M., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Andluh F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A., Jalali M., Kaluuh F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A., Liux X., Matles B., McIntcoh T.C., McLeod M.P., McPherson D., Lasko P., Lei Y., Levitsky A.A., I.J. J., Liz., Liang Y., Lin X., Lausko P., Lei Y., Levitsky A.A., Noules M. P., Mczhecz M. D., Mont S., Mullshina N.V., Mozarry C., Moriecod M.P., Puri V., Reese M.G., Ralason K.A., Nixon K., Nusskern D.R., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shen B.C., Siden-Kaaman D.A., Weinsern D.R., Wang S., Yan R., Shul R., Savirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinsey G.M., Weissenbach J., Wang K.H., Shong K.M., Now W., Zhou K., Zho S., Zhan M., Zhong G., Zhao Q., Zhao Q., Zhao G., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=22456065; PubMed=12537568;

MEDLINE=22456065; PubMed=12537568;

Geoliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pefeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Filishing a whole-genome shotqun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Ratel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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EMBL, AL834168, CAHlOG86.1; .. InterPro; IPR001360; Glyco hydro 1.
InterPro; IPR010979; Ribosomal HZTH.
PROSITE; PS00572; GLYCOSYL HYDROL FI I, UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  EMBL; AE003520; AAF49253.2; -...
FlyBase; FEQURO36795; CG18231.1.
GO; GO:0016706; F:oxidoreductase activity, acting on paired GO; GO:0019538; P:protein metabolism; IEA.
InterPro; IPR006620; Pro_4_hyd_alph.
SEQUENCE 435 A4Hc; 1. OFB957AS0F29AD34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 57.3%; Score 47; DB 2; Length 1122; Local Similarity 61.5%; Pred. No. 73; es 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                   2; Length 435;
                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122 AA; 129234 MW; AEF46E21E18614FF CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update).
MKIAA1840 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q69YG6;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence upd
25-OCT-2004 (TrEMBLrel. 28, Last annotation up
4ypothetical protein DKFZp762B1512 (Fragment)
Name=DKFZp762B1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1580 AA.
                                                                                                                                                                                                                                                                                                57.3%; Score 47; DB
80.0%; Pred. No. 29;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 LTPYPKLKTALFP 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The German cDNA Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKPFPKLKVEVFP 13
                                                                                                                                                                                                                                                                                                                               Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 FPKLKISVFP 404
                                                                                                                                                                                                                                                                                                                                                                                                                           4 FPKLKVEVFP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryonic tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=mKIAA1840
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NON TER
SEQUENCE
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Matches
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Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                    P 11.

SEQUENCE FROM N.A.

SECOTORICE FROM N.A.

Sato Y., Fukuda Y., Hirano H.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO71627; BA568273.1; -.

R Gramene, O948M2; --

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R InterPro; IPR005540; KNOXI.

R InterPro; IPR005541; KNOXI.

R InterPro; IPR005541; KNOXI.

R Pfam; PF03790; KNOXI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 159;
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Sato Y., Fukuda Y., Hirano H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB071658; BAB663304.1; -.
EMBL, AB071660; BAB68306.1; -.
EMBL, AB071661; BAB68307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 AA; 16897 MW; 48753DB82F95AC16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.1%; Score 46; DB 2;
53.3%; Pred. No. 15;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.1%; Score 46; DB 2; 53.3%; Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR005540; KNOX1.
InterPro; IRR005541; KNOX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKPFPKLKVEVFPFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza rufipogon (Wild rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKPFPKLKVEVFPFP 15
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Best Local Similarity 53.3
Matches '8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Pfam; PF03791; KNOX2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 8; Conserv
Oryza meridionalis
                                                                                                                         NCBI_TaxID=40149;
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Matches
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Q93VC5
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STITE DE REPERENTANT SON CONTRACTOR 
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                   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Nagase T., Ohara O., Koga H.;
Frediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologues
CDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
EMBL; AK129453; BAC98263.1; -.
GO; GO:000384; F:caralytic activity; IEA.
GO; GO:000199; F:ferric iron binding; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Magase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new CDNA clones from brain which code for large proteins in vitro.";
EMBL; AB059743; BAB47469.2;
InterPro; IPR0011065; Myb DNA binding.
PROSITE; PS00152; GLYCOSYL HYDROL F1; UNKNOWN 1.
PROSITE; PS00037; MYB 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazaa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.3%; Score 47; DB 2; Length 1580;
llarity 61.5%; Pred. No. 1e+02;
Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           1580 AA; 178755 MW; EDF5BAAA8DD8CD76 CRC64;
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01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
10-OCT-2003 (TEMBLrel. 25, Last annotation update)
Transcription factor OSH3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
KIAAA1840 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=21245130; PubMed=11347906;
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1120 LTPYPKLKTALFP 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LTPYPKLKAALFP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 61.5*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LKPFPKLKVEVFP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
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PubMed=14621295;
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SEQUENCE
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SEQUENCE
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Q948M2
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Q96JI7
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Oryza barthii.
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza glaberrima (African rice).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.1%; Score 46; DB 2; Length 161; Best Local Similarity 53.3%; Pred. No. 15; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Sato Y., Fukuda Y., Hirano H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071628; BAB68274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato Y., Fukuda Y., Hirano H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071626; BAB68272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AA; 17116 MW; ECEA5658836DBA30 CRC64;
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                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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GO; GO:0005G4; C:nucleus; IEA.
GO; GO:0003G77; F:DNA binding; IEA.
InterPro; IPR005540; KNOX1.
Fam; PF03790; KNOX1, 1.
Pfam; PF03791; KNOX2; 1.
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Gramene; 0948M3; -.
GO; 00:0003673; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR005540; KNOXI.
FEAM; PP03790; KNOXI; 1.
Pfam; PP03791; KNOXI; 1.
Pfam; PP03791; KNOXI; 1.
NON_TER 161 161
SEQÜENCE 161 AA; 17116 MW; ECEASÉ
                                                                                                                                                                                                             Q948M1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Transcription factor OSH3 (Fragment)
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                                                                                                                                                                              PRT;
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| ||||: |:|: |
19 LLPFPKVSVQVYTVP 33
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                                                                                                                                                                              PRELIMINARY;
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                                                                                                                      RESULT 10
0948M1
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                                  셤
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                                                                                                                                                                        dryza sativa (indica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza glumipatula.
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
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53.3%; Pred. No. 15;
ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Sato Y., Fukuda Y., Hirano H.;
Submitred (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071642; BAB68288.1; -.
EMBL; AB071653; BAB68299.1; -.
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Sato Y., Fukuda Y., Hirano H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071629; BAB68275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 161
161 AA; 17174 MW; DOCODGIC8369FA77 CRC64;
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                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
C1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Transcription factor OSH3 (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transcription factor OSH3 (Fragment).
   161 AA
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR005540; KNOX1.
InterPro; IPR005541; KNOX2.
Pfam; PF03790; KNOX1; I.
Pfam; PF03791; KNOX2; I.
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19 LLPFPKVSVQVYTVP 33
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Best Local Similarity 53.3.
Best Local Similarity 53.3.
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Best Local Similarity 53.3
Matches 8; Conservative
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   PRELIMINARY;
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Pfam; PF03791; KNOX2; 1
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/ Match 56.1%; Score 46; DB 2; Length 164; Local Similarity 53.3%; Pred. No. 16; as 8; Conservative 3; Mismatches 4; Indels
                                                                                                                   164 164 17403 MW; 430B9D3BAF43C6C5 CRC64;
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SEQUENCE FROM N.A.
Sato Y., Fukuda Y., Hirano H.;
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19 LLPFPKVSVQVYTVP 33
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LLPFPKVSVQVYTVP 33
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Best Local Similarity 53.3.
Best Local 8; Conservative
                        InterPro; IPR005541; KNO)
Pfam; PF03790; KNOX1; 1.
Pfam; PF03791; KNOX2; 1.
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Q948L6
ID Q948L6
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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56.1%; Score 46; DB 2; Length 161; 53.3%; Pred. No. 15; ive 3; Mismatches 4; Indels
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Sato Y., Fukuda Y., Hirano H.;
Submitrded (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO71631; BAB68276.11; -.
EMBL; ABO71635; BAB68281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Sato Y., Fukuda Y., Hirano H.;
Submitted (EEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071625; BAB68271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AA; 17248 MW; 3E4D33040B16B866 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transcription factor OSH3 (Fragment).
                                                                                                                                                                                                                                                          163 AA
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GO; GO; 0005G4; C:nucleus; IEA.
GO; GO; 0003G77; F:DNA binding; IEA.
InterPro; IPR005540; KNOX1.
InterPro; IPR005541; KNOX2.
Pfam; PP03790; KNOX1; 1.
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GO; GO:0003677; F:DNA binding; IEA.
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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Oryza sativa (Rice)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sato Y., Fukuda Y., Hirano H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071662; BAB68308.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 AA; 17432 MW; 945B9D2936C8D45C CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transcription factor OSH3 (Fragment).
                           0948L6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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53.3%; Pred. No. 16;
tive 3; Mismatches
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Go; 000:005634; c:nucleus; IEA.
Go; Go:0003677; F:DNA binding; IEA.
InterPro; IPR005540; KNOX1.
InterPro; IPR005541; KNOX2.
Pfam; PP03790; KNOX1; 1.
Pfam; PP03791; KNOX2; 1.
PRT;
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Search completed: April 12, 2005, 08:05:50 Job time: 73.1818 secs